

## **FIGURE 1**

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGCTGGTAAGGATTACAAAAGGTGCAGGTATG  
AGCAGGTCTGAAGACTAACATTGTGAAGTTGTAACAGAAAACCTGTTAGAAATGGGTGGT  
TTCAGCAAGGCCTCAGTCCTCCTCAGCCCTGTAATTGGACATCTGCTGCTTCATATTT  
TCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTACCTTATATCAGTGACACTGG  
TACAGTAGCTCCAGAAAAATGCTTATTGGGCAATGCTAAATATTGCGGCAGTTTATGCATTG  
CTACCATTTATGTCGTATAAGCAAGTTCATGCTCTGAGTCCTGAAGAGAACGTTATCATCAA  
TTAAACAAGGCTGGCCTTGACTTGAATACTGAGTTAGGACTTCTATTGTGGCAAACCTT  
CCAGAAAACAACCCTTTGCTGCACATGTAAGTGGAGCTGTGCTTACCTTGGTATGGCTCAT  
TATATATGTTGTCAGACCACCTTCTACCAAATGCAGCCAAAATCCATGGCAAACAAAGTC  
TTCTGGATCAGACTGTTGGTTATCTGGTGTGGAGTAAGTGCACCTAGCATGCTGACTTGCTC  
ATCAGTTTGACAGTGGCAATTGGACTGATTAGAACAGAAAACCTCCATTGAAACCCGAGG  
ACAAAGGTTATGTGCTTCACATGATCACTACTGCAGCAGAATGGTCTATGTCATTCTCTT  
GGTTTCTGACTTACATTGATTTGAGAAAATTCTTACGGGTGGAAGCCAATTACA  
TGGATTAACCCCTATGACACTGCACCTGCCCTATTAAACATGAACGAACACGGCTACTTCCA  
GAGATATTGATGAAAGGATAAAATATTCTGTAATGATTGATTCTCAGGGATTGGGAAAGG  
TTCACAGAAGTTGCTTATTCTCTGAAATTCAACCACTTAATCAAGGCTGACAGTAACACT  
GATGAATGCTGATAATCAGGAAACATGAAAGCCATTGATAGATTATTCTAAAGGATATCAT  
CAAGAAGACTATTAAAACACCTATGCCTATACTTTTATCTCAGAAAATAAGTCAAAAGACT  
ATG

## **FIGURE 2**

<subunit 1 of 1, 266 aa, 1 stop

<MW: 29766, pI: 8.39, NX(S/T): 0

MWWFQQGLSFLPSALVIWTSAAFIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAV  
LCIATIYVRYKQVHALSPEENVIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSGAVLTFG  
MGSLYMFVQTILSYQMOPKIHGKQVFIRLLLVIWCGVSALSMLTCSVLHSGNFGTDLEQKLHW  
NPEDKGYVLHMITTAAEWSMSFSFFGFLTYIRDFQKISLRVEANLHGLTLYDTAPCPINNERTR  
LLSRDI

**Important features:**

**Type II transmembrane domain:**

amino acids 13-33

**Other Transmembrane domains:**

amino acids 54-73, 94-113, 160-180, 122-141

**N-myristoylation sites.**

amino acids 57-63, 95-101, 99-105, 124-130, 183-189

### **FIGURE 3**

CGGACGCGTGGCGGACGCGTGGGGAGAGCCGAGTCCCGCTGCAGCACCTGGAGAAGGCAGACC  
GTGTGAGGGGGCCTGTGGCCCCAGCGTGTGCGCTCGGGAGTGGAAAGTGGAGGCAGGAGCCTTC  
CTTACACTTCGCCATGAGTTTCCATCGACTCCAGCATCATGATTACCTCCAGATACTATTTTG  
GATTTGGGTGGCTTCTCATGCGCAATTGTTAAAGACTATGAGATACTGAGTCAGTATGTTGTACAG  
GTGATCTCTCCGTGACGTTGCATTTCTGCACCATGTTGAGCTCATCATCTTGAAATCTTAGG  
AGTATTGAATAGCAGCTCCCGTTATTTCACTGGAAATGAACCTGTGTGTAATTCTGCTGATCCTGG  
TTTCATGGTGCCTTTACATTGGCTATTTATTGTGAGCAATATCCGACTACTGCATAAACACGA  
CTGCTTTTCTGTCTTATGGCTGACCTTATGTATTCTCTGGAAACTAGGAGATCCCTTCC  
CATTCTCAGCCAAAACATGGATCTTATCCATAGAACAGCTCATGCCGTTGGTGTGATTGGAG  
TGACTCTCATGGCTCTTCTGGATTGGTGTCACTGCCATACACTTACATGTCTTACTTC  
CTCAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATATGAT  
CATAAAGCAAAAGAAAAGGATGGCAATGGCACGGAGAACAAATGTTCCAGAAGGGGAAGTGCATAACA  
AACCATCAGGTTCTGGGAATGATAAAAAGTGTACCACTCAGCATCAGGAAGTGAAGATCTTACT  
CTTATTCAACAGGAAGTGGATGCTTGGAAAGAATTAAGCAGGCAGCTTTCTGGAAACAGCTGATCT  
ATATGCTACCAAGGAGAGAATAGAATACTCCAAACCTTCAAGGGAAATATTTAATTTCCTGGTT  
ACTTTTCTCTATTACTGTGTTGGAAATTTCATGGCTACCATCAATATTGTTTGATCGAGTT  
GGGAAAACGGATCTGTACAAGAGGCATTGAGATCACTGTGAATTATCTGGAAATCCAATTGATGT  
GAAGTTTGGTCCAACACATTCCTCATCTGGTGAATAATCATCGTCACATCCATCAGAGGAT  
TGCTGATCACTCTAACCAAGTCTTTATGCCATCTAGCAGTAAGTCTCCAATGTCATTGCTCTG  
CTATTAGCACAGATAATGGCATGTACTTGTCTCTGTGCTGATCCGAATGAGTATGCCTT  
AGAATACCGCACCATTAATCACTGAAGTCTGGAGAACACTGCAGTTCAACTCTATCACCGTTGGTTG  
ATGTGATCTCCTGGTCAGCGCTCTCTAGCATACTCTTCTCTATTGGCTCACAAACAGGCACCA  
GAGAAGCAAATGGCACTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGTGGTTCAAAATTAA  
GATATAAGAGGGGGAAAATGGAACCAGGGCTGACATTTATAAAACAAACAAATGCTATGGTAGC  
ATTTTCACCTTCATAGCATACTCCTCCCGTCAGGTGATACTATGACCATGAGTACCATCAGCCAG  
AACATGAGAGGGAGAGAACTAACTCAAGACAATACTCAGCAGAGAGCATCCGTGTGGATATGAGGCTGG  
TGTAGAGGCGGAGAGGAGCCAAGAAACTAAAGGTGAAAATACACTGGAACCTGGCAAGACATGT  
CTATGGTAGCTGAGCCAACACGTTAGGATTCGTTTAAGGTTCACATGGAAAGGTTAGCTTGC  
CCTTGAGATTGACTCATTAAATCAGAGACTGTAACAAAAAAAAGGGCGGCCGCG  
ACTCTAGAGTCGACCTGCAGAAGCTGGCCCATGGCCAACCTGTTATTGCAGCTATAATG

## **FIGURE 4**

MSFLIDSSIMITSQILFFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEILGV  
LNSSSRYFHWKMNLCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTMYFFWKLGDP  
FPILSPKHHGILSIEQLISRVGVIGVTLMAILSGFGAVNCPTYMSYFLRNVTDDILALERRLQ  
TMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQQEVDALEELSRQ  
LFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVFDRVGKTDPVTRGIEI  
TVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAISSSKSSNVIVLLAQMIMGMY  
FVSSVLLIRMSMPLERYRTIITEVLGELQFMFYHRWFDVIFLVSALSSILFLYLAHKQAPEKQMAP

**Important features:**

**Signal peptide:**

amino acids 1-23

**Potential transmembrane domains:**

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,  
425-444

**N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246

**Eukaryotic cobalamin-binding proteins**

amino acids 151-160

## FIGURE 5

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTAACATAGTTCC  
AGAACTCTCATCCGACTAGTTATTGAGCATCTGCCTCTATATCACCAAGTGGCCATCTGAGGT  
GTTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGGCTTCTCACT  
TCCATCTGGACCAAGGGCTCTGGTCAAGGCTTTGCGTGCAGAAGAGCTTCCATCCAGGT  
GTCATGCAGAATTATGGGGATCACCCCTGTGAGCAAAAAGGCGAACCGAGCTGAATTTCACAG  
AAGCTAAGGAGGCCCTGAGGCTGCTGGGACTAAGTTGCCGGCAAGGACCAAGTTGAAACAGCC  
TTGAAAGCTAGCTTGAAACTTGCACTATGGCTGGGAGATGGATTGTTGCTGATCTCTAG  
GATTAGCCAAACCCCAAGTGTGGAAAAATGGGGTGGGTCTGATTGAAAGGTTCCAGTGA  
GCCGACAGTTGCAGCCTATTGTTACAACACTCATCTGATACTTGGACTAACTCGTGCATTCCAGAA  
ATTATCACCAACAAAGATCCCATATTCAACACTCAAACGTCAACACAAACAGAATTATG  
CAGTGCAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTACTACTCCTC  
CTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAAATTGATTGTCACAGAAGTTTATG  
GAAACTAGCACCATGTCTACAGAAACTGAACCAATTGTTGAAAATAAGCAGCATTCAGAATGA  
AGCTGCTGGTTGGAGGTGTCCCCACGGCTCTGCTAGTGCTCTCTCTTGGTGTG  
CAGCTGGCTTGATTTGCTATGTCAAAGGTATGTAAGGGCTTCCCTTTACAAACAAGAAT  
CAGCAGAAGGAAATGATCAGAACAAAGTAAGGAGAAGGGCAATGATAGCAACCTAA  
TGAGGAATCAAAGAAAATGATAAAACCAAGAAGTCAAGAGTCAAGCAAAACTACCGTGC  
GATGCCCTGGAAGCTGAAGTTAGATGAGACAAATGAGGAGACACACCTGAGGCTGGTTCTT  
CATGCTCCCTACCCCTGCCCAAGCTGGGAAATCAAAGGCCAAAGAACCAAAGAAGAAAGTCA  
CCCTGGTTCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGGAAAT  
GCCCTTCTCCTTATGTAACCCCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCT  
TTCTAGGCTGGCTATGCTTAATAATATCCACTGGGAGAAAGGAGTTGCAAAGTGCAGGAC  
CTAAAACATCTCATCAGTATCCAGTGGTAAAAGGCCCTGGCTGTGAGGCTAGGTGGTTG  
AAAGCCAAGGAGTCAGTGAGACCAAGGCTTCTACTGATTCCGAGCTCAGACCCCTTCTCA  
GCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCCTCTGAGGCCGTAAGAGCAAAAGAAT  
GGCAGAAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTGTAAA  
GCTAAAATAAGAAATAGAACAGGCTGAGGATACGACAGTACACTGTCAGCAGGACTGTAAAC  
ACAGACAGGGTCAAAGTGTCTCTGAACACATTGAGTTGAATCACTGTTAGAACACACACA  
CTTACTTTCTGGTCTCTACCACTGCTGATATTTCTAGGAAATAACTTTACAAGTAACA  
AAAATAAAAATCTTATAAAATTCTATTCTGAGTTACAGAAATGATTACTAAGGAAGATT  
ACTCAGTAATTGTTAAAAGTAATAAAACATTTGCTGAATAGCTACTATATGTC  
AAAGTGTGTGCAAGGTATTACACTCTGTAATTGAATTATTCTCAGCTTATCTACTTCCAAACTAAT  
AACGCTATCTGGGAAGCTATTCTTCTGAGTTGATATTCTAGCTTATCTACTTCCAAACTAAT  
TTTATTTGCTGAGACTAATCTTATTCTCATTTCTCATATGGCAACCATTATAACCTTAATT  
TATTATAACATACCTAAGAAGTACATTGTTACCTATACCAAAAGCACATTAAAAGTGC  
ATTAACAAATGTATCACTAGCCCTCTTTCAACAAAGAAGGGACTGAGAGATGCAGAAATATT  
TGTGACAAAAATTAAAGCATTTAGAAAACCTT

## **FIGURE 6**

MARCFSLVLLTSIWTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTAKEACRLLG  
LSLAGKDQVETALKASFETCSYGVGDGFVVISRISPNCGKNGVGVLIWKPVSRQFAAYCYN  
SSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTPPAPASTSIPR  
RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGFCKVK  
RYVKAFFPTNKNQQKEMIETKVVKEEKANDSNPNEESKTDKNPEESKSPSKTTVRCLEAEV

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

**Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

**Tyrosine kinase phosphorylation site.**

amino acids 79-88

**N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## **FIGURE 7**

CGCCGCGCTCCCGCACCGCGGGCCGCCACCGCGCCGCTCCGCATCTGCACCCGCAGCCCCGGC  
GCCCTCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCGAGCGCAACTCGGTCCAGTCGGGGCGG  
CGGCTGCGGGCGCAGAGCGGAGATGCAGCGCTTGGGGCCACCCCTGCTGTGCTGCTGCTGGCGG  
CGGCGGTCCCCACGGCCCCCGGCCCGCTCCGACGGCACCTCGGCTCCAGTCAGCAGCCGGCGG  
GCTCTCAGCTACCCGAGGAGGCCACCTCAATGAGATGTTCCGAGGGTTGAGGAAGTGT  
GGAGGAACACGCAAAATTGCGCAGCGCGGTGGAAGAGATGGAGGCAGAAGAAGCTGCTGCTA  
AAGCATCATCAGAAGTGAACCTGGCAAACCTACCTCCAGCTATCACAATGAGACCAACACAGAC  
ACGAAGGTTGAAATAATACCATCCATGTGACCGAGAAATTCAAGATAACCAACAACCAGAC  
TGGACAATGGTCTTTCAGAGACAGTTACATCTGTGGGAGACAGAAGAAGGCAGAAGGAGCC  
ACGAGTGCATCATCGACGAGGAAGTGTGGGCCAGCATGTAAGTGCAGTTGCCAGCTCCAGTAC  
ACCTGCCAGCCATGCCGGGGCAGAGGATGCTCTGCACCCGGGACAGTGAAGTGTGAGACCA  
GCTGTGTCTGGGGTCACTGCACCAAAATGGCCACCAGGGGAGCAATGGGACCATCTGTGACA  
ACCAGAGGGACTGCAGCCGGGCTGTGCTGTGCTTCAGAGAGGGCTGCTGTCCCTGTG  
ACACCCCTGCCGTGGAGGGCGAGCTTGCATGACCCGCCAGCCGGCTCTGGACCTCATCAC  
CTGGGAGCTAGAGCTGTGGAGCCTGGACCGATGCCCTGTGCTGCAGTGGCCTCCCTGTG  
CCCACAGCCACAGCCTGGTGTATGTGCAAGCCGACCTTGTGCTGGGAGCCGTGACCAAGATGG  
GAGATCCTGCTGCCAGAGAGGTCCCCGATGAGTATGAAGTTGCCAGCTTCATGGAGGAGGTG  
CCAGGAGCTGGAGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCCTGGGGAGCCGTG  
CCGCCGCTGCACTGCTGGAGGGGAAGAGATTAGATCTGGACAGGCTGTGGTAGATGTG  
TAGAAATAGCTAATTATTCAGGTGCTTAGGCGTGGGCTGACAGGCTTCTCT  
CATCTCTCCAGTAAGTTCCCTCTGGCTGACAGCATGAGGTGTTGCAATTGTTCA  
CCCCCAGGCTGTTCTCCAGGCTCACAGTCTGGTGTGCTGGGAGAGTCAGGCAGGGTTAAACTG  
GGAGCAGTTGCCACCCCTGTCAAGATTATGGCTGCTTGCCCTACAGTTGCCAGACAGCC  
TTTGTCTACATGGCTTGATAATTGTTGAGGGAGGAGATGAAACAATGTGGAGTCTCC  
TGATTGGTTGGGAAATGTGGAGAAGAGTGCCTGCTTGCAACATCAACCTGGAAAAATG  
CAACAAATGAATTTCACGCAGTTCCATGGCATAGGTAAAGCTGTGCTCAGCTGT  
AGATGAAATGTTGTTCAACCTGCATTACATGTGTTATTCACTCCAGCAGTGTGCTCAGCT  
TACCTCTGTGCCAGGGCAGCATTTCATATCAAGATCAATTCCCTCTCAGCACAGCCTGG  
AGGGGTCATTGTTCTCCTCGCCATCAGGGATCTCAGAGGCTCAGAGACTGCAAGCTGCT  
CAAGTCACACAGCTAGTGAAGACCAGAGCAGTTCATCTGGTGTGACTCTAAGCTCAGTGT  
CTCCACTACCCCACACCAGCCTGGTGCACCAAAAGTGTCTCCAAAAGGAAGGAGAATGG  
TTTCTGAGGCATGCACATCTGAATTAGGTCAAACATCTCACATCCCTCTAAAGTAAA  
CTACTGTTAGGAACAGCAGTGTCTCACAGTGTGGGAGCCGTCTTCTAATGAAGACAATG  
ATTGACACTGTCCTCTTGGCAGTTGCAATTGAAAGGTATATGACTGAGCGTAGCA  
TACAGGTTAACCTGCAGAACAGTACTTAGGTAAATTGTAGGGCGAGGATTATAATGAAATTG  
AAAATCACTTAGCAGCAACTGAAGACAATTATCAACCACTGAGGAAAATCAAACCGAGCAGGG  
TGTGTGAAACATGGTGTAAATTGCGACTGTCGCAACTGAACTCTACGCCACTCCACAAATG  
TTTCAGGTGTCACTGGACTGTTGCCACCATGTATTCACTCCAGAGTTCTTAAAGTTAAAGT  
CATGATTGTATAAGCATGCTTCTTGAGTTAAATTATGTATAAACATAAGTTGCATTAG  
ATCAAGCATAAATCACTCAACTGCACAAAAA  
AAAAAAAAAAAAAAAAAAAAA

## **FIGURE 8**

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQHKL  
RSAVEEMEAEEAAAKASSEVNLNLPPSYHNETNTDTKVNNTIHVHREIHKITNNQTGQMVFSE  
TVITSGVDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRQMLCTRSECCGDQLCVWGHC  
TKMATRGNSNGTICDNQRDCQPGLCCAFQRGLLFPVCTPLPVEGELCHDPASRLLDLITWELEPDG  
ALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEVGSFMEEVRQELEDLE  
RSLTEEMALGEPAAAAALLGGEI

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

**Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

**N-myristoylation site.**

amino acids 202-208, 217-223

**Amidation site.**

amino acids 140-144

## **FIGURE 9**

CGGACGCGTGGCGGACGCGTGGGGCTGTGAGAAAGTCCAATAAATACATCATGCAACCCAC  
GGCCCACCTTGTGAACTCCTCGCCAGGGCTGATGTGCGTCTTCAGGGCTACTCATCCAAG  
GCCTAATCCAACGTTCTGTCTCAATCTGCAAATCTATGGGTCTGGGGCTTCTGGACCTT  
AACTGGGTACTGGCCCTGGCCAATGCGTCTCGCTGGAGCCTTGCCTCCTACTGGCCTT  
CCACAAGCCCCAGGACATCCCTACCTCCCTTAATCTCGCTTCATCCGACACTCCGTTACC  
ACACTGGGTCATTGGCATTGGAGCCCTCATCCTGACCCTTGTGCAGATAGCCCGGTCATCTTG  
GAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCGTAGCCCCTGCATGTGCTGTTT  
CAAGTGCTGCCTCTGGTGTCTGGAAAAAATTATCAAGTCTAAACCGCAATGCATACATCATGA  
TCGCCATCTACGGGAAGAATTCTGTCTCAGCCAAAATGCGTCATGCTACTCATGCGAAC  
ATTGTCAGGGTGGTGTCTGGACAAAGTCACAGACCTGCTGCTGTCTTGGGAAGCTGCTGGT  
GGTCGGAGGCGTGGGGCTCTGCTTCTCCGGTGCATCCGGGGCTGGTAAAG  
ACTTTAAGAGCCCCCACCTCAACTATTACTGGCTGCCATCATGACCTCCATCTGGGGCCTAT  
GTCATGCCAGCGGCTCTCAGCTTTCCGGCATGTGTGGGACACGCTCTCCCTGCTTCT  
GGAAGACCTGGAGCGGAACAAACGGCTCCCTGGACCGCCCTACTACATGTCCAAGAGCCTCTAA  
AGATTCTGGCAAGAAGAACGAGGCGGGGGACAACAAGAAGAGGAAGAAGTGACAGCTCCGG  
CCCTGATCCAGGACTGCACCCCCACCCCCACCGTCCAGGCATCCAACCTCATTGCCTTACAGGT  
CTCCATTGTGGTAAAAAAAGGTTTAGGCCAGGCGGGTGGCTACGCCTGTAATCCAACACT  
TTGAGAGGCTGAGGCGGGGCGGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGCCAACATGGTG  
AAACCTCCGTCTATTAAAAAATACAAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCACTCC  
GCTACTCGGGAGGCTGAGGCAGGGAGAATCGCTGAACCCGGAGGCAGAGGTTGCAGTGAGCCGA  
GATCGGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAAACAAA  
AAGATTTATTAAAGATATTGTAACTC

## **FIGURE 10**

RTRGRTRGGCEKVPINTSCNPTAHVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVGLFWTL  
NWVLALGQCVLAGAFASFYWAFHKPQDIPFPLISAFIRTLRYHTGSLAFGALILTLVQIARVIL  
EYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLRNAYIMIAIYGKNFCVSAKNAFMLLMRN  
IVRVVVLVDKVTDLFFFGLVVGVGVLSSFFSGRIPGLGKDFKSPHLNYYWLPIMTSILGAY  
VIASGFFSVFGMCVDTLFLCFLEDLERNNNGSLDRPYYMSKSLLKILGKKNEAPPDNKKRKK

**Important features:**

**Transmembrane domains:**

amino acids 57-80 (type II), 110-126, 215-231, 254-274

**N-glycosylation sites.**

amino acids 16-20, 27-31, 289-293

**Hypothetical YBR002c family proteins.**

amino acids 276-288

**Ammonium transporters proteins.**

amino acids 204-231

**N-myristoylation sites.**

amino acids 60-66, 78-84

**Amidation site.**

amino acids 306-310

## **FIGURE 11**

CCCCCGCGCCCGGCCGGCGCCGGCGCCGAAGCGGGAGCCACCGCCATGGGGCCTGCCTGGAGCCTGC  
TCCCTGCTCAGCTGCCTGCCTGCCTCTGCCTGCATCTGTGCAGCTGCTGCCCGC  
CAGCCGCAACTCCACCGTGAGCCGCCTCATCTTCAGTTCTTCTCTTCTGGGGTGCTGGTGTCCA  
TCATTATGCTGAGCCGGCGTGAGAGTCAGCTACAAGCTGCCCTGGTGTGAGGAGGGGCC  
GGGATCCCCACCGTCTGCAGGGCACATCGACTGTGGCTCCCTGCTTGGCTACCGCGCTGTCTACCG  
CATGTGCTCGCCACGGCGGCCTCTTCTTACCCCTGCTCATGCTCTGCGTGAGCAGCA  
GCCGGGACCCCCGGGCTGCCATCCAGAATGGTTTGGTCTTAAGTTCTGATCCTGGTGGCCTC  
ACCGTGGGTGCCTTACATCCCTGACGGCTCTTACCAACATCTGGTCTACTTCGGCGTGTGG  
CTCCTTCTCTTACATCCTCATCCAGCTGGTGTGCTCATCGACTTGCCTACTGGAAACCAGCGGT  
GGCTGGGCAAGGCCGAGGAGTGGGATTCCCGTGCCTGGTACGCAGGCCCTTCTTCACTCTCCTC  
TTCTACTTGCTGTCGATCGCGGCCGTGGCGTGTGTTACTACACTGAGCCCAGCGCTGCCA  
CGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTCTGTGTCTGCGTCCATGCTGCTGTCTGC  
CCAAGGTCCAGGACGCCAGCCCAACTGGGTCTGCTGCAGGCCCTGGTCATCACCTCTACACCATG  
TTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCAACCCCCATTGCCAACCCAGCT  
GGGCAACGAGACAGTTGGCAGGCCCGAGGGCTATGAGACCCAGTGGTGGGATGCCCGAGCATTG  
TGGGCCATCATCTCCCTCTGTCACCCCTTTCATCAGTCTGCGCTCTCAGACCACGGCAGGTG  
AACAGCCTGATGCAGACCGAGGAGTCCCACCTATGCTAGACGCCACACAGCAGCAGCAGCAGGT  
GGCAGCCTGTGAGGCCGGGCTTGAACAAGCAGCAGGCCGTACCTACAGCTACTCTTCTCC  
ACTTCTGCCTGGTGTGGCTACTGCACGTCTGATGACGCTCACCAACTGGTACAAGCCGGTGAG  
ACCCGGAAGATGATCAGCACGGACCCGCGCTGTGGGTGAAGATCTGTGCCAGCTGGCAGGGCTGCT  
CCTCTACCTGGACCCCTGGTAGCCCCACTCCTCTGCGCAACCGCAGCTCAGCTGAGGCAGCCTCA  
CAGCCTGCCATCTGGTGCCTCTGCCACCTGGTGCCTCTGGCTCGGTGACAGCAACCTGCCCTC  
CCCACACCAATCAGCCAGGCTGAGCCCCACCCCTGCCAGCTCCAGGACCTGCCCTGAGCCGGC  
CTTCTAGTCGTAGTGCCTCAGGGTCCGAGGAGCATCAGGCTCTGCGAGAGCCCCATCCCCCGCCAC  
ACCCACACGGTGGAGCTGCCCTCCCTCCCCCTCCCTGTTGCCCATACTCAGCATCTGGATGAA  
AGGGCTCCCTGTCTCAGGCTCCACGGAGCAGGGCTGCTGGAGAGAGCAGGGGAACCTCCACACAG  
TGGGGCATCCGGCACTGAAGCCCTGGTGTTCCTGGTCACGTCCCCAGGGACCCCTGCCCTTCTG  
GACTTCGTGCCTTACTGAGTCTAAGACTTTCTAATAAACAAAGCCAGTGCCTGTAAAAAAA

## **FIGURE 12**

MGACLGACSLSCASCLCGSAPCILCSCCPASRNSTVSRLIFTFFLFLGVLVSIIMLSPGVESQL  
YKLPWVCEEGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFTLLMLCVSSSRDPRAAIQ  
NGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSLFILQLVLLIDFAHSWNQRWLGKAE  
ECDSRAWYAGLFFFLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFCVCVSIAAVLPKV  
QDAQPNSGLLQASVITLYTMFTWSALSSIPEQKCNPHLPTQLGNETVVAGPEGYETQWWDAPSI  
VGLIIFLLCTLFISLRSSDHRQVNSLMQTECOPMLDATQQQQQQVAACEGRAFDNEQDGVTYSY  
SFFHFCLVLASLHVMMTLTNWYKPGTRKMISTWTAVWVKICASWAGLLLYLWTILVAPLLLNRD  
FS

**Signal sequence:**

amino acids 1-20

**Transmembrane domains:**

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,  
272-283, 324-340, 391-406, 428-444

### **FIGURE 13**

CGGGCCAGCCTGGGGCGGCCAGGAACCACCCGTTAAGGTGTCTCTTTAGGGATGGTGA  
GGTTGGAAAAAGACTCCTGTAACCCTCCTCCAGGATGAACCACCTGCCAGAAGACATGGAGAACG  
CTCTCACCGGGAGCCAGAGCTCCATGCTCTCGCGAATATCCATTCCATCAACCCCACACAA  
CTCATGCCAGGATTGAGTCCTATGAAGGAAGGGAAAGAAAGGCATATCTGATGTCAGGAGGAC  
TTTCTGTTGTTGTCACCTTGACCTTATTGTAACATTACTGTGGATAATAGAGTTAAATG  
TGAATGGAGGCATTGAGAACACATTAGAGAAGGAGGTGATGCAGTATGACTACTATTCTTCATAT  
TTTGATATATTCTCTGGCAGTTTCGATTTAAAGTGTAAACTTGCATATGCTGTGCAG  
ACTGCGCCATTGGTGGGCAATAGCGTTGACAACGGCAGTGACCAGTGCCTTTACTAGCAAAG  
TGATCCTTCGAAGCTTCTCTCAAGGGGCTTGGCTATGTGCTGCCATCATTCACTC  
CTTGCCTGGATTGAGACGTGGTCCTGGATTCAAAGTGTACCTCAAGAACAGAAGAAAA  
CAGACTCCTGATAGTTCAGGATGCTCAGAGAGGGCAGCACTTACCTGGTGGCTTCTGATG  
GTCAGTTTATTCCCTCCTGAATCGAACAGGATCTGAAGAACGCTGAAGAAAAACAGGACAGT  
GAGAAACCACTTAGAACATAGTACTACTTTGTTAAATGTGAAAAACCTCACAGAAAGTC  
ATCGAGGCACAAAGAGGCAGGCAGTGGAGTCCCTGTCGACAGTAAAGTGAATGGTACGTC  
CACTGCTGGCTTATTGAACAGCTAATAAGATTATTGTAATACCTCACAAACGTTGTAC  
CATATCCATGCACATTAGTGCCTGCCTGGCTGGTAAGGTAATGTGATTCATCCTCT  
TCAGTGAGACTGAGCCTGATGTGTTAACAAATAGGTGAAAGAAAGTCTGTGCTGTATTCTAATC  
AAAAGACTTAATATATTGAAGTAACACTTTTAGTAAGCAAGATACTTTTATTCAATTCA  
AGAATGGAATTTTTGTTCATGTCTCAGATTATTTGTATTTCTTTAACACTCTACATT  
TCCCTGTTTTAACTCATGCACATGTGCTCTTGTACAGTTTAAAGTGTAAATAAAACTG  
ACATGTCAATGTGGCTAGTTTATTCTGTTGCATTATGTGATGGCTGAAGTGTGGA  
CTTGCAAAAGGGGAAGAAAGGAATTGCGAACATGTAAAATGTCACCAGACATTGTATT  
TTATCATGAAATCATGTTCTGATTGTTCTGAAATGTTCTAAATACTCTTATTGAAATGC  
ACAAAATGACTTAAACCATTCATATCATGTTCTTGCAGCCAATTCAATTAAAATGAA  
CTAAATTAAAAA

## **FIGURE 14**

MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESTYEGREKKGISDVRRTFCLFVTFDLLF  
VTLLWIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLLAYAVCRLRHWWAIALT  
AVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPOEAEEENRLLIVQDASER  
AALIPGGLSDGQFYSPPESEAGSEEAEEKQDSEKPLLEL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-20

**Transmembrane domains:**

amino acids 54-72, 100-118, 130-144, 146-166

**N-myristoylation sites.**

amino acids 14-20, 78-84, 79-85, 202-208, 217-223

## **FIGURE 15**

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCCTGGGCCGACCCGCCAGGAAAGACTGAGG  
CCGCGGCCCTGCCCCGGCTCCCTGCGCCGCCGCCCTCCCAGGACAGAAGATGTGCTCAG  
GGTCCCTCTGCTGCTGCCGCTGCTCTGCTACTGGCCCTGGGCCCTGGGTGCAGGGCTGCCAT  
CCGGCTGCCAGTGCAGCCACAGACAGTCTTCTGCACTGCCGCCAGGGGACACGGTGCC  
CGAGACGTGCCACCCGACACGGTGGGCTGTACGTCTTGAGAACGGCATCACCAGTGCACGC  
AGGCAGCTTGCGGCCCTGCCGGGCTGCAGCTCTGGACCTGTACAGAACAGATGCCAGCC  
TGCCCAGCGGGCTTCCAGCCACTGCCAACCTCAGAACCTGGACCTGACGCCAACAGGCTG  
CATGAAATACCAATGAGACCTCCGTGGCTGCGGCCCTCGAGGCCCTACCTGGCAAGAA  
CCGCATCCGCCACATCCAGCCTGGCTGCCCTCGACACGCTGACCGCCCTCTGGAGCTCAAGCTGC  
AGGACAACGAGCTGCCGGACTGCCCGCTGCCCTGCCCGCTGTGCTGCTGGACCTCAGC  
CACAAACAGCCTCTGGCCCTGGAGCCGCATCTGGACACTGCCAACGTGGAGGGCTGCC  
GGCTGGCTGGGCTGCGAGCTGGACGAGGGCTCTCAGCCGCTGCGAACCTCCACGACC  
TGGATGTGTCCGACAACCAGCTGGAGCGAGTGCCACCTGTATCCGAGGCCTCCGGGCTGACG  
CGCCTGCCGCTGGCGCAACACCCGATTGCCAGCTGCCGCCAGGACCTGGCGGCCCTGGC  
TGCCCTGAGGAGCTGGATGTGAGCAACCTAAGCCTGAGGCCCTGCCCTGGGAGCCTCTGGGCC  
TCTTCCCCCGCCTGCCGCTGCTGGCAGCTGCCGCCAACCCCTCACTGCGTGTGCCCTGAGC  
TGGTTGGCCCTGGGTGCGCAGAGGCCACGTACACTGCCAGCCCTGAGGAGACGCCGCTGCCA  
CTTCCCCGCAAGAACGCTGGCCGCTGCTCTGGAGCTGACTACGCCGACTTGGCTGCCAG  
CCACCAACACCACAGCCACAGTGCCAACACAGGAGGCCCTGGTGGGAGGCCACAGCCTGTCT  
TCTAGCTGGCTCTACCTGGCTAGCCCCACAGGCCGCAACTGAGGCCAGGCCCTC  
CACTGCCAACCGACTGTAGGGCTGTCCCCAGGCCAGTGCCACCGTCCACCTGCC  
ATGGGGCACATGCCACCTGGGACACGGCACCTGGCTGCTGTGCCCTGAAGGCTTCACG  
GGCCTGACTGTGAGAGGCCAGATGGGGCAGGGGACAGGCCAGGCCCTACACAGTCAGGCC  
GCCACCACGGTCCCTGACCTGGGATCGAGCGGTGAGGCCACCTCCCTGCCGCTGGGCTG  
AGCGCTACCTCCAGGGAGCTCCGTGAGCTCAGGACTGCCCTCGCTCGCTGAGTACACGGTCA  
GGCCCTGATAAGCGGCTGGTACGCTGCCACTGGGACACGGCACCTGGCTGCTGTGCC  
GCTGCCGCCCCAACCCACTTACCCGCTGTGTCATGCCCTTGGGCCCCGGGGTGCCGGAGG  
GCCAGGAGGCCCTGCCGGGAGGGCAACTGCCGCTCCTCATGGCCGCCCTGCCGCGGTG  
CAGGGCCGAGGGCAACTGCCGCTCCTCATGGCCGCCCTGCCGCGGTG  
GCTGGCTGCCGCTGGGCACTGCCGCTCCTCATGGCCGCCCTGCCGCGGTG  
ACAAAGGGCAAGGTGGGGCAGGGCTGGGGCCCTGGAACTGGAGGGAGTGAAGGT  
CCAGGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGGGCTG  
ACTCATGGCTTCCCAGGGCTGGCCTCCAGTCACCCCTCCACGCAAAGCC  
GAGAGAGACAGGGAGCTGGGCCGGCTCTCAGCCAGTGAAGATGCC  
ACACCAACGTAAGTCTCAGTCCAACCTGGGATGTGCA  
GGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCATCTGTGAGATG  
CTGAGCTGGCCAGCTGCCCTGCCCTGCCCTGCCCAACGTG  
CTGGCAGGGCCCTGCCATGTGCTGGTAACG  
TCCAGGGGACCCCTGGGGCCAGTGAAGGAAGCT  
GGCTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGA  
TTAGGAACATTTTAAATATATATTATAAGAGAT  
GGGAAGATGTTTCAA  
GGCCTTTGTAAGAAAAA  
APP\_ID=10063532

## **FIGURE 16**

MCSRVPLLLPLLLLALGPGVQGCPSCQCSQPQTVCFTARQGTTVPRDVPPDTVGLYVFENGIT  
MLDAGSFAGLPGLQQLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLRRLERLY  
LGKNRIRHIQPGAFDTLDRLLEKLQDNELRALPPLRIPRLLLLDLSHNSLLALEPGILDGTANVE  
ALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDL  
AGLAALQELDVSNLSQLALPGDLSGLFPRLLAARNPFCNCVCPLSWFGPWVRESHVTLASPEE  
TRCHFPPKNAGRLLLELDYADFGCPATTTATVPTTRPVREPTALSSSLAPTWLSPTAPATEAP  
SPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHACLCPEGFTGLYCESQMGQGTRPSPTP  
VTPRPPRSLTGLIEPVSPSTLRVGLQRYLQGSSVQLRSRLTYRNLSGPDKRLVTLRLPASLAEY  
TVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAV  
LLAALAAVGAAVCVRGRAMAAAQDKGQVGPAGPLELEGVKVPLEPGPKATEGGGEALPSGSE  
CEVPLMGFPGPGLQSPHLAKPYI

**Important features:**

**Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 579-599

**EGF-like domain cysteine pattern signature.**

amino acids 430-442

**Leucine zipper pattern.**

amino acids 197-219, 269-291

**N-glycosylation sites.**

amino acids 101-105, 117-121, 273-277, 500-504, 528-532

**Tyrosine kinase phosphorylation sites.**

amino acids 124-131, 337-345

**N-myristoylation sites.**

amino acids 23-29, 27-33, 70-76, 142-148, 187-193, 348-354,  
594-600, 640-646

## FIGURE 17

GCAGCGCGAGGCAGCGGTGGCTGAGTCGTGGCAGAGCGAAGGCACAGCTCATGCG  
GGTCGGATAGGGCTGACGCTGCTGTGCGGTGCTGAGCTTGGCTCGCGTCCGG  
ATGAAGAAGGCAGCCAGGATGAATCCTAGATTCAAGACTACTTGACATCAGATGAGTCAGTA  
AAGGACCAACTACTGCAGGCAGAGTAGTTGCTGGTCAAATATTCTGATTCAAAGAAATCTGA  
ATTAGAATCCTCTATTCAAGAAGAGGAAGACAGCCTCAAGAGCCAAGAGGGGGAAAGTGTACAG  
AAGATATCAGCTTCTAGACTCCTCAAATCCAGAAAACAAGGACTATGAAGAGCCAAGAAAGTA  
CGGAAACCAGCTTGACGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTTCCCTTCT  
TTTCCTAGATAAGGAGTATGATGAATGTACATCAGATGGAGGGAAAGATGGCAGACTGTGGTGTG  
CTACAACTATGACTACAAAGCAGATGAAAAGTGGGGCTTTGTGAAACTGAAGAAGAGGCTGCT  
AAGAGACGGCAGATGCAGGAAGCAGAAATGATGTATCAAACCTGGAAATGAAAATCTTAATGGAAG  
CAATAAGAAAAGCCAAAAAGAGAAGCATATCGGTATCTCCAAAAGGCAGCAAGCATGAACCATA  
CCAAAGCCCTGGAGAGAGTGTATGCTCTTTATTGGTGATTACTGCCACAGAATATCCAG  
GCAGCGAGAGAGATGTTGAGAAGCTGACTGAGGAAGGCCTCCCAAGGGACAGACTGCTCTGG  
CTTTCTGTATGCCTCTGGACTTGGTGTAAATTCAAGTCAGGCAAAGGCTTGTATATTATACAT  
TTGGAGCTTGGGGCAATCTAATAGCCCACATGGTTTGGTAAGTAGACTTTAGTTGAAGGCT  
AATAATATTAACATCAGAAGAATTGTGGTTATAGCGGCCACAACCTTTTCAAGCTTCTGATGATC  
CAGATTGCTGTATTAAGACCAAATATTCAAGTGAACCTCCTCAAATTCTGTTAATGGATAT  
AACACATGGAATCTACATGAAATGAAAGTGGTGGAGTCCACAATTCTTAAATGATTAG  
TTGGCTGATTGCCCTAAAAAGAGAGATCTGATAAAATGGCTCTTTAAATTCTGAGTTG  
GAATTGTCAGAATCATTTCACATTAGATTATCATAATTAAAAATTCTTAGTTTCA  
AAATTGTAAATGGTGGCTATAGAAAAACACATGAAATATTATAACATTTGCAACAAATGC  
CCTAAGAATTGTTAAATTCACTGGAGTTATTGTGAGATGACTCCAGAGAGCTACTTCTG  
TTTTTACTTTCATGATTGGCTGTCTCCATTCTGGTCAATTGCTAGTGTGACACTGT  
GCCTGCTTCCAGTAGTCTCATTTCCATTGGCTAAATTGTTACTTTCTTGCTAATTGG  
AAGATTAACCTTTAATAAAATTATGCTAAGATTAaaaaaaaaaaaaaaaaaaaaaaa  
aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa

## **FIGURE 18**

MRVRIGLTLLLCAVLLSLASASSDEEGSQDESLDSTTLTSDESVKDHTTAGRVVAGQIFLDSEEESEL  
ESSIQEEEDSLKSQEGESVTEDISFLESPNPNKDYEEPKKVRKPALTAIEGTAHGEPCHFPLFLDK  
EYDECTS DGDREDGRLWCATTYDYKADEKWGFCETEEEAKRRQMQEAEMMYQTGMKILNGSNKKSQKR  
EAYRYLQKAASMNHTKALERVSYALLFGDYLQPQNIQAAREMFEKLTEEGSPKGQTALGFLYASGLGVN  
SSQAKALVYYTFGALGGNLIAHMVLVSRL

**Important features:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 195-199, 217-221, 272-276

**Tyrosine kinase phosphorylation site.**

amino acids 220-228

**N-myristoylation sites.**

amino acids 120-126, 253-259, 268-274, 270-274, 285-291, 289-295

**Glycosaminoglycan attachment site.**

amino acids 267-271

**Microbodies C-terminal targeting signal.**

amino acids 299-303

**Type II fibronectin collagen-binding domain protein.**

amino acids 127-169

**Fructose-bisphosphate aldolase class-II protein.**

amino acids 101-119

## **FIGURE 19**

AATTCAAGATTTAACGCCATTCTGCAGTGGAAATTCACTGAACAGACTAGCAAGAGGACACCACCTTCTT  
GTATTATAACAAGAAAGGAGTGTACCTATCACACACAGGGGGAAAAATGCTCTTTGGGTGCTAGG  
CCTCCTAATCCTCTGGTTCTGTGGACTCGTAAAGGAAAACAAAGATTGAAGACATCACTG  
ATAAGTACATTTTATCACTGGATGTGACTCGGGCTTGGAAACTTGGCAGCCAGAACTTTGAT  
AAAAAGGGATTCATGTAATCGCTGCCGTGACTGAATCAGGATCAACAGCTTAAAGGCAGA  
AACCTCAGAGAGACTCGTACTGTGCTTCTGGATGTGACCGACCCAGAGAATGTCAAGAGGACTG  
CCCAGTGGGTGAAGAACCAAGTGGGGAGAAAGGTCTCTGGGTCTGATCAATAATGCTGGTGT  
CCCGCGTGTGGCTCCCCTGACTGGCTGACACTAGAGGACTACAGAGAACCTATTGAAGTGAA  
CCTGTTGGACTCATCAGTGTGACACTAAATATGCTCCTTGGTCAAGAAAGCTCAAGGGAGAG  
TTATTAAATGTCTCCAGTGTGGAGGTGCCCTGCAATCGTGGAGGGGCTATACTCCATCCAAA  
TATGCAGTGGAAAGGTTCAATGACAGCTTAAGACGGGACATGAAAGCTTGGTGTGCACGTCTC  
ATGCATTGAACCAGGATTGTTCAAAACAAACTGGCAGATCCAGTAAAGGTAAATTGAAAAAAAC  
TCGCCATTGGGAGCAGCTGTCTCCAGACATCAAACAATATGGAGAAGGTTACATTGAAAAA  
AGTCTAGACAAACTGAAAGGCAATAATCTATGTGAACATGGACCTCTCCGGTGGTAGAGTG  
CATGGACCACGCTCTAACAGTCTTCCCTAACACTCATTATGCCGCTGGAAAAGATGCCAAA  
TTTCTGGATACCTCTGTCTCACATGCCAGCAGCTTGCAGACTTTTATTGGTAAACAGAAA  
GCAGAGCTGGCTAACCCAGGAGTGTGACTCAGCTAACCAATGTCTCCTCCAGGCTATGA  
AATTGGCCGATTTCAAGAACACATCTCCTTCAACCCATTCTTATCTGCTCCAACCTGGACT  
CATTAGATCGTGTCTTGGATTGCAAAAGGAGTCCCACCATCGCTGGTGTATCCAGGGT  
CCCTGCTCAAGTTCTTGGAAAGGAGGCTGGATGGTACATCACATAGGCAAGTCCCTGCCCT  
GTATTTAGGCTTGCCTGCTTGGTGTGATGTAAGGAAATTGAAAGACTTGCCATTCAAATGA  
TCTTACCGTGGCTGCCATGCTATGGCCCCAGCATTACAGTAACCTGTGAATGTTAAGT  
ATCATCTCTTATCTAAATATTAAGATAAGTCAACCCAAAAAA  
AAAAAA

## **FIGURE 20**

MLFWVLGLLILCGFLWTRKGKLKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIACLTESG  
STALKAETSERLRTVLLDVTDPENVKRTAQWVKNQVGEKGLWGLINNAGVPGVLAPTDWLTLEDY  
REPIEVNLFGLISVTLNMLPLVKKAQGRVINSSVGGRLAIVGGGYTPSKYAVEGFNDSLRRDMK  
AFGVHVSCIEPGLFKTNLADPVKVIEKKLAIWEQLSPDIKQQYGEFYIEKSLDKLGNKSYVNMD  
LSPVVECMDHALTSLFPKTHYAGKDAKIFWIPLSHMPAALQDFLLLKQKELANPKAV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 136-152

**N-glycosylation sites.**

amino acids 161-163, 187-190 and 253-256

**Glycosaminoglycan attachment site.**

amino acids 39-42

**N-myristoylation sites.**

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

## **FIGURE 21**

CTGAGGC GGCGGTAGCATGGAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTGTGCTCGGCG  
CACTCGCTTCAGCACCTCAACACGGACTCGGACACCGAAGGTTCTTCTGGGAAGTAAAA  
GGTGAAGCCAAGAACAGCATTACTGATTCCAAATGGATGATGTTGAAGTTGTTATACAATTGA  
CATTCAAGAAATATATTCCATGCTATCAGCTTTAGCTTTATAATTCTTCAGGCGAAGTAAATG  
AGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGTTGGTACAAATTCCGT  
CGTCATTCAAGATCAGATCATGACGTTAGAGAGAGGCTGCTTCACAAAAACTTGCAAGGAGCATT  
TTCAAAACCAAGACCTTGTCTGCTATTAAACACCAAGTATAAAACAGAAAGCTGCTCTACTC  
ATCGACTGGAACATTCTTATATAAACCTCAAAAAGGACTTTACAGGGTACCTTAGTGGTT  
GCCAATCTGGGCATGCTGAACAACACTGGGTATAAAACTGTATCAGGTTCTGTATGTCACACTGG  
TTTAGCCGAGCAGTACAAACACACAGCTCTAAATTTGAAGAACATGGATCCTAAAGGAGG  
TACATAAGATAAAATGAAATGTATGCTTCATTACAAGAGGAATTAAAGAGTATATGCAAAAAGTG  
GAAGACAGTGAACAAGCAGTAGATAAAACTAGTAAAGGATGTAACACAGATTAAACGAGAAAATTGA  
GAAAAGGAGAGGAGCACAGATTAGGCAGCAAGAGAGAAGAACATCCAAAAGACCTCAGGAGA  
ACATTTCTTGTCAAGGCATTACGGACCTTTTCCAAATTCTGAATTTCATTCACTGTGTT  
ATGTCTTAAAAAATAGACATGTTCTAAAGTAGCTGTAACTACAACCACATCTCGATGTAGT  
AGACAATCTGACCTTAATGGTAGAACACACTGACATTCCCTGAAGCTAGTCAGCTAGTACACCAC  
AAATCATTAAGCATAAACGCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTGGTTGTTA  
GATACACAAGACAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAACATCCAAAAT  
GAGCAGCCCAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTGGTGAATATTACGGTCTC  
CTACATTTGATCTTTAACCTTACAAGGAGATTTTTATTGCTGATGGTAAAGCAAAAC  
ATTCTATTGTTTACTATGAGCTACTGAGTAAGTTCAATTGTTTACTATGTTCAAC  
TGTTGAGTAATACACAGATAACTCTTAGTGCATTACTTCACAAAGTACTTTCAAACATCA  
GATGCTTTATTCCAAACCTTTTACCTTCACTAAGTTGAGGGAAAGGCTTACACAG  
ACACATTCTTGAATTGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAATCCCAGCACT  
TAGGGAAGACAAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCCTGGCAACGTATT  
GAGACCATGTCTATTAAAAAATGAAAAGCAAGAATAGCCTTATTCAAATATGGAAA  
GAAATTATGAAAATTCTGAGTCATTAAATTCTCCTTAAGTGTAAACTTTTAAAGAGTA  
CATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCAATAATTGCAAAACATCATCT  
AAAATTAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 22**

MEGESTSAVLSGFVLGALAFQHLNTSDTEGFLLGEVKGEAKNSITDSQMDDVEVVYTIDIQKYI  
PCYQLFSFYNSSGEVNEQALKKILSNVKNNVGWYKFRRHSDQIMTFRERLLHKNLQEHFSNQDL  
VFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVGSCMSTGFSRAV  
QTHSSKFFED GSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGA  
QIQAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSSCNYNHHLDVVDNLTL  
MVEHTDipeASPASTPQIIKHKALDLDDRWFQKRSRLLTQDKRSKANTGSSNQDKASKMSSPET  
DEEIEKMKGFGEYSRSPTF

**Important features:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation sites.**

amino acids 75-79, 322-326

**N-myristoylation site.**

amino acids 184-154

**Growth factor and cytokines receptors family.**

amino acids 134-150

## **FIGURE 23**

GGCACAGCCGCGCGCGGAGGGCAGAGTCAGCCGAGCCAGTCCAGCGGAGCAGCGGACCAGCCAGGGCAGCCAA  
GCAGCGCGCAGCGAACGCCGCCGCCACACCCCTCGCGTCCCGCGCCCTGCCACCCCTCCCTCCTCCCC  
GCGTCCCCGCCCTCGCGGCCAGTCAGCTTGCCGGTTCGCTGCCCGGAAACCCCGAGGTCAACCGCCGCCCT  
GCTTCCCTGGGCCGCGGCCCTCCACGCCCTCCTCTCCCGCTGCCCCGGCGCTGGCACCGGGGACCGTGCCTGA  
CGCGAGGCCAGCTACTTTCGCCCGCTCTCCCGCTGCTCGCTCTTCAACCAACTCCAACCTCCTCTCCC  
TCCAGCTCCACTCGCTAGTCCCCGACTCCGCCAGCCCTCGGCCGCTGCCGTAGGCCGTTCCCGTCCGGTCCAAA  
GGTGGGAACCGTCCGCCCGGCCCGCACCAATGGCACGGTCGGCTTGCCGCTCTGCACCCGGCAGTGCCT  
AGGCCGCCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGAAGTGCAGCTTTACGTGTCCAAAGGCTTC  
AACAGAACGATGCCCTCCACGAGATCAACGGTATCATTGAAGATCTGCCCCAGGGTTACCTGCTGCTCT  
CAAGAGATGGAGGAGAAGTACAGCCTGCAAGAATGATTCAAAGTGTGGTCAGCGAACAGTGAATCATTG  
CAAGCTGCTTGTCTCACGTTACAAGAAGTTGATGAATTCTCAAAGAACTACTGAAAATGAGAGAAATCCCTG  
AATGATATGTTGTGAAGACATATGGCCATTATACATGCAAAATCTGAGCTATTAAAGATCTCTCGTAGAGTTG  
AAACGTTACTACGTGGGGAAATGTAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCCTCTGGAGCGGATG  
TTCCGCTGGTAACCTCCAGTACCACTTACAGATGAGTATCTGGAATGTTGAGCAAGTACGGAGCAGCTGAAG  
CCCTTCGGAGATGTCCTCGCAAATTGAAGCTCCAGGTTACTCGTGTCTTTGTAGCAGCCGTACTTCGCTCAAGGC  
TTAGCGGTTGCGGGAGATGTCGTGAGCAAGGTCTCCGTGGTAACCCACAGCCAGTGTACCCATGCCCTGTTGAAG  
ATGATCTACTGTCCTCACTGCCGGGTCTCGTGAECTGTGAACCCATGTTACAACACTACTGCTCAAACATCATGAGAGGC  
TGTGTTGGCCAACCAAGGGATCTGATTTGAATGGAACAAATTCTAGATGCTATGCTGATGGTGGCAGAGAGGCTA  
GAGGGTCTTTCAACATTGAATCGGTATGGATCCCATCGATGTAAGATTCTGATGCTATTATGAACATGCAGGAT  
AATAGTGTCAAGTGTCTCAGAAGGTTTCCAGGGATGTTGAGCCCTCCAGCTGGACGAATTCTCGT  
TCCATCTCTGAAAGTGCCTCAGTGTCTCGTTCAAGACCACATCCCCGAGGAACGCCAACACAGCAGCTGGCACT  
AGTTTGGACCGACTGGTTACTGATGTCAGGAGAACTGAAACAGGCCAGAAATTCTGGCTCCCTCCGAGCAAC  
GTTTGCAACGATGAGAGGATGGCTGAGGAAACGCCAATGAGGATGACTGTTGAATGGAAAGGCCAAAGCAGGTAC  
CTGTTGGCAGTGACAGGAAATGGATTAGCCAACCAGGGCAACAACCCAGGGTCCAGGTTGACACCAGCAAACAGAC  
ATACTGATCTCTCGCAAATCATGGCTCTTCAGTGTGATGACCAGCAAGATGAAAGATGCAACATGGGACGACGTG  
GACTTCTTGATATCAGTGTGAAAGTAGTGGAGAAGGAAGTGGAAAGTGGCTGTGAGTATCAGCAGTGCCTTCAGAG  
TTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCTGAGAAAGCCGACAGTGTGTTGCTGGTCTGGCA  
CAGGCCAACCTCTCACTGTCTCTGCATCTGTTCTGGTTATGCAAGAGAGAGTGGAGATATTCTCAAACACTGAG  
AAAAAGTGTCAACAAAGTAAAGGGCACCAGTTACCTTACCTGACTTTGCTTTAAATGAA  
TGGACAACATGTACAGTTTACTATGTTGCACTGGTTAAGAAGTGTGACTTTGTTCTCATTGAGTTGGG  
AGGAAAAGGGACTGTGCATTGAGTTGGTCTGCTCCCCAAACCATGTTAACAGTGGCTAACAGTGTAGGTACAGAA  
CTATAGTTAGTTGTGCATTGTGATTCTACTCTATTATTTGTTGATGTTTTCTCATTGTTGTTGGT  
TTTTTTCCAACGTGTGATCTGCCATTGTTCTTACAACCAAACCGGGTCCCTTGGCACGTAACATGTACGTATT  
TCTGAAATATTAAAGTGTACAGAAGCAGGTTTATTTATCATGTTATCTTAAAGAAAAAGCCAAAAAGC

## **FIGURE 24**

MARFGLPALLCTLAVLSAALLAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQGST  
CCSQEMEEKYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSNDMFVKTYGH  
LYMQNSELFKDLFVELKRYYVGVNLEEMLNDFWARLLERMFRLVNSQYHFTDEYLECVSKYTE  
QLKPGDGVPRKLKLQVTRAFVAARTFAQGLAVAGDVSKVSVNPTAQCTHALLKMIYCSHCRLG  
VTVKPCNYCSNIMRGCLANQGDLDFEWNNFIDAMLMVAERLEGPFNIESVMDPIDVKISDAIMN  
MQDNSVQVSQKVFOQCGPPKPLPAGRISRSISESAFSARFRPHHPEERPTTAAGTSLDRLVTDVK  
EKLKQAKKFWSLPSNVNCNDERMAAGNGNEDDCWNGKGKSRYLFAVTGNGLANQGNPENVQVDT  
KPDILILRQIMALRVMTSKMKNAYNGNDVFFDISDESSGEGSGSGCEYQQCPSEFDYNATDHAG  
KSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

**Important features:**

**Signal peptide:**

amino acids 1-22

**ATP/GTP-binding site motif A (P-loop).**

amino acids 515-524

**N-glycosylation site.**

amino acids 514-518

**Glycosaminoglycan attachment sites.**

amino acids 494-498, 498-502

**N-myristoylation sites.**

amino acids 63-69, 224-230, 276-282, 438-444, 497-503, 531-537

**Glycans proteins.**

amino acids 54-75, 105-157, 238-280, 309-346, 423-460, 468-506

## **FIGURE 25**

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCTGAC  
CTGAGTCATCCCCAGGGATCAGGAGCCTCAGCAGGGAACCTCCATTATATTCTTCAAGCACT  
TACAGCTGCACCGACAGTTGCGGAAAGTTCTAATCTTCCCTCCTGTTGCTGCCACTAA  
TGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGTGCAGAGGCCACAGGGACCGAGGC  
CAGGCTCTAGGAGATGGCTCCAGGAAGGCGGCAAGAATGTGAGTGCAAAGATTGGTCCTGAG  
AGCCCCGAGAAGAAAATTCATGACAGTGTCTGGCTGCCAAAGAAGCAGTGCCCCTGTGATCATT  
TCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGAAAGCCAACAAGCATTCCAGA  
GCCTGCCAGCAATTCTCAAACAATGTCAAGAAGCTTGCTGCTGCCTTG**TAGGAGCTCG**  
AGCGCCCACTTCCAATTAAACATTCTCAGCCAAGAACAGTGAGCACACCTACCAGACACTC  
TTCTTCTCCCACCTCACTCTCCACTGTACCCACCCCTAAATCATTCCAGTGCCTCAAAAGCA  
TGTTTTCAAGATCATTGTTGCTCTCTAGTGTCTCTCGTCAGTCTTAGCCT  
GTGCCCTCCCTACCCAGGCTAGGCTTAATTACCTGAAAGATTCCAGGAAACTGTAGCTTCC  
AGCTAGTGTCAATTAAACCTAAATGCAATCAGGAAAGTAGCAAACAGAAGTCAATAAATTTT  
AAATGTCAAAAAAAAAAAAAAAA

## **FIGURE 26**

MKVLISSLLLLPLMLMSMVSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRRKFM  
TVSGLPKKQCPCDHFKGNNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

**Important features:**

**Signal peptide:**

amino acids 1-22

**N-myristoylation sites.**

amino acids 27-33, 46-52

## **FIGURE 27**

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTCCCCAGCGGAAGCACAGCTAG  
AGCTGGTCTGCCATGGACATCCTGGTCCCACCTCTGCAGCTGCTGGTCTGCTTACCTGCC  
CCTGCACCTCATGGCTCTGCTGGCTGCTGGCAGCCCTGTGCAAAGCTACTTCCCTACCTGA  
TGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAGCTTCAGCAG  
ATAAAGGGCTTACAGGAGCCTCCGGAAAGTGGCCTACTGGAGCTGGCTGCGGAACCGGAGC  
CAACTTCAGTTCTACCCACCAGGCTGCAGGGCACCTGCCTAGACCCAAATCCCCACTTGAGA  
AGTTCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATATGAGCGGTTGTGGTGGCTCCT  
GGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGTGGTGGCTGCACTCTGGTGTG  
CTCTGTGCAGAGCCAAGGAAGGTCTGCAGGAGGTCCGGAGAGTACTGAGACCCGGAGGTGTG  
TCTTTTCTGGGAGCATGTGGCAGAACCATATGAAAGCTGGGCTTCATGTGGCAGCAAGTTTC  
GAGCCCACCTGAAACACATTGGGATGGCTGCTGCCCTACCAGAGAGACCTGGAAGGATCTGA  
GAACGCCAGTTCTCGAAATCCAATGGAACGACAGCCCCCTCCCTGAAGTGGCTACCTGTTG  
GGCCCCACATCATGGGAAAGGCTGTCAAACAATCTTCCAAGCTCCAAGGCACACTTGTCC  
TTCCCCAGCCTCCAATTAGAACAGCCACCCACCAGCCTATCTATCTCCACTGAGAGGGACCTA  
GCAGAAATGAGAGAACACATTGATGTACCACTACTAGTCCCTCTCTCCCAACCTCTGCCAGGG  
AATCTCAACTTCAATCCGCCCTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGG  
AAACACTAGGACCCCTGTTGTATCCTCAACTGCAAGTTCTGGACTAGTCTCCCAACGTTGCCTC  
CCAATGTTGTCCTTCCCTCGTCCATGGTAAAGCTCCTCTCGCTTCCCTGAGGCTAC  
CCATGCGTCTCTAGGAACCTGGTACAAAAGCTAGGTGCCTGCATCCCTGCCAAGCCCCCTGAC  
CCTCTCTCCCACTACCACCTCTTCTGAGCTGGGGCACCAGGGAGAATCAGAGATGCTGGG  
ATGCCAGAGCAAGACTCAAAGAGGCAGAGGTTTGTCTCAAATTTTTAATAATAGACGAA  
ACCACG

## **FIGURE 28**

MDILVPPLLQLLVLLTLPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSQIKGL  
TGASGKVALLELGCGTGANFQFYPPGCRVTCLDPNPHFEKFLTKSMAENRHLQYERFVVVAPGEDM  
RQLADGSMDVVVCTLVLCVQSPRKVLQEVRVLRPGGVLFWEHVAEPYGSWAFMWQQVFEPTW  
KHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLPGPHIMGKAVKQSFPSKALICSFPSL  
QLEQATHQPIYLPLRGT

**Important features:**

**Signal peptide:**

amino acids 1-23

**Leucine zipper pattern.**

amino acids 10-32

**N-myristoylation sites.**

amino acids 64-70, 78-84, 80-86, 91-97, 201-207

## **FIGURE 29**

CAATGTTGCCTATCCACCTCCCCAAGCCCCTTACCTATGCCTGCTGCTAACGCTGCTGCTGCT  
GCTGCTGCTGCTAAAGGCTCATGCTGGAGTGGGACTGGTCGGTGCCAGAAAGTCTCTCTG  
CCACTGACGCCCATCAGGGATTGGGCCTCTTCCCCCTTCCTGTGTCCTGCCTCAT  
CGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGAAGGGGAGAAAGTGGGGATGGCTA  
AGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGTGGCTAGGGGGCTGCCTTATTAAA  
GTGGTTTTATGATTCTTACTAATTACAAAGATATTAAGGCCCTGTTCATTAAGAAATT  
GTTCCCTTCCCTGTGTTCAATGTTGTAAAGATTGTTCTGTGTAAATATGTCTTATAATAAAC  
AGTTAAAAGCTGAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 30**

MLLLTLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTC SQAQPRG  
EGEKVGDG

**Important features:**

**Signal peptide:**

amino acids 1-15

**Growth factor and cytokines receptors family:**

amino acids 3-18

## **FIGURE 31**

GTTCGAATTCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCAAGTT  
CCTCCAAGCAAGTCATTCCCTTATTAACCGATGTGTCCCTAAACACCTGAGTGCTACTCCCT  
ATTTGCATCTGTTGATAAATGATGTTGACACCCCTCCACCGAATTCTAAGTGGATCATGTCGG  
GAAGAGATAACAATCCTTGGCTGTATCCTCGCATTAGCCTTGTCTTGGCCATGATGTTACC  
TTCAGATTCATCACCAACCCCTCGGTTCACATTTCATTGGTTATTTGGGATTGTTGTT  
TGTCTGCGGTGTTTATGGTGGCTGTATTATGACTATACCAACGACCTCAGCATA  
GAATTGGGAAATATGAAGTGCCTGCTGGGTTGCTATCGTATCCACAGGCATCACGGCAGTG  
CTGCTCGTCTTGATTTGTTCTCAGAAAGAGAATAAAATTGACAGTTGAGCTTTCAAATCAC  
AAATAAAGCCATCAGCAGTGCTCCCTCCTGCTGTTCCAGCCACTGTGGACATTGCCATCCTCA  
TTTCTCTGGTCCCTGGGTGGCTGTGCTGAGCCTGGAACTGCAGGAGCTGCCAGGTT  
ATGGAAGGCAGGCAAGTGGAAATATAAGCCCCTTCCGGCATTGGTACATGTGGTGTACCATTT  
AATTGGCCTCATCTGGACTAGTGAATTCATCCTGCGTGCCAGCAAATGACTATAGCTGGGCAG  
TGGTTACTGTTATTCAACAGAAGTAAAAATGATCCTCTGATCATCCATCCTCGTCCTC  
TCCATTCTCTCTTACCATCAAGGAACCGTTGTGAAAGGGTATTAAATCTCTGTTGAG  
GATTCCGAGAACATTGTACATGCAAAACGACTGAAAGAACAGCAGCATGGTGCATTGT  
CCAGGTACCTGTCGATGCTGACTGCTGTTCTGGTCTTGACAAAATACCTGCTCCATCTC  
AACAGAACATGACATACACTACAACGCTATTAAATGGACAGATTCTGTACATCAGCAAAGATGC  
ATTCAAAATCTTGTCCAAGAACACTCAAGTCACCTTACATCTATTAAACTGCTTGAGACTTCATAA  
TTTTCTAGGAAAGGTGTTAGTGGTGTGTTCACTGTTGGAGGACTCATGGCTTTAACTAC  
AATCGGGCATTCCAGGTGTGGCAGTCCCTCTGTTATTGGTAGCTTTGGCCTACTTAGTC  
CCATAGTTTTATCTGTGTTGAAACTGTGCTGGATGCACCTTCCCTGTGTTGCTGTTGATC  
TGGAAACAAATGATGGATCGTCAAGAACCCCTACTTATGGATCAAGAATTCTGAGTTGTA  
AAAAGGAGCAACAAATTAAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAGGAATGAGGA  
GGGAACAGAACCTCAGGCCATTGTGAGATAGATAACCCATTAGGTATCTGTACCTGGAAAACATT  
TCCTCTAAGAGCCATTACAGAAATAGAAGATGAGACCACTAGAGAAAAGTTAGTGAATT  
TTAAAAGACCTAATAACCCATTCTCCTCAAA

## **FIGURE 32**

MSGRDTILGLCILALALSIAMMFTFRFITTLLVHIFISLVLVILGLLFVCGVLWWLYYDYNLDSIE  
LDTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISAPFLLFQPLWTFA  
ILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFILACQOMTIA  
GAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVMMQNALKQQHG  
ALSRYLFRCYCFCFWCLDKYLLHQNAYTTAINGTDFCTSAKDAFKILSKNSSHFTSINCFGD  
IIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPLLLVAFFAYLVAHSFLSVFETVLDALFLCFA  
VDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNAQQDKHSLRNEEGTELQAIVR

**Important features:**

**Signal peptide:**

amino acids 1-20

**Putative transmembrane domains:**

amino acids 35-54, 75-97, 126-146, 185-204, 333-350, 352-371

**N-glycosylation sites.**

amino acids 204-208, 295-299, 313-317

**N-myristoylation sites.**

amino acids 147-153, 178-184, 196-202, 296-275, 342-348

## **FIGURE 33**

TTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTGGACCTCCTGTTCTCCCTAGA  
ATAATTGTATGGGATTGTGATGCAGGAAGCCTAAGGGAAAAGAATATTCTGTTCTGTTCTG  
GAAAATTGGAAAAAAATTGCTCTTCAAAACAAGGGTGTATTCTGATATTATGAGGAC  
TGTTGTTCTCACTATGAGGCATCTGTTATTGAAATGTCCTGTTGCTGGTACTGGAGTAC  
ATTCAAACAAAGAAACGGCAAAGAAGAGATTAAAAGGCCAAGGTTCACTGTGCCTCAGATCAACTGC  
GATGTCAAAGCCGAAAGATCATCGATCCTGAGTTCTGAAATGTCAGCAGGATGCAAAGA  
CCCCAAATACCATGTTATGGCACTGACGTGTTATGCATCCTACTCCAGTGTGTTGGCCTGCCG  
TACACAGTGGTGTGCTTGATAATTCAAGGAGGAAAATACTTGTGCGAAGGTTGCTGGACAGTCT  
GGTTACAAAGGGAGTTATTCAACGGTGTCCAATGTTATCCCTACACGATGGAGAGAAATCCTT  
TATCGTCTTAGAAAGTAAACCCAAAAGGGTGTAACTTACCCATCAGCTCTTACATACTCATCAT  
CGAAAAGTCCAGCTGCCAAGCAGGTGAGACCACAAAGCCTATCAGAGGCCACCTATTCCAGGG  
ACAACGTGACAGCCGGTCACTGTGATGCGAGCTCTGGCTGTCACTGTAGCTGTGCCACCCCCAC  
CACCTGCCAAGGCCATCCCTCTGCTGCTTCTACCACAGCATCCCCAGACCACAAATCAGTGG  
GCCACAGGAGCCAGGAGATGGATCTCTGGTCACTGCCACCTACAAAGCAGCCAAACAGGCC  
AGAGCTGATCCAGGTATCAAAGGCAAGATCTTCAGGAGCTGCCCTCCAGAAACCTGTTGGAGC  
GGATGTCAGCCTGGGACTTGTCCAAAAGAAGAATTGAGCACACAGTCTTGGAGCCAGTATCCC  
TGGGAGATCCAAACTGCAAATTGACTGTGTTTATTGATGGAGCACCAGCATTGGCAAA  
CGGCAGATTCCGAATCCAGAAGCAGCTCTGGCTGATGTTGCCAAGCTTGTACATTGGCCCTGC  
CGGTCCACTGATGGGTGTTGTCAGTATGGAGACAACCTGCTACTCACTTTAACCTCAAGACAC  
ACACGAATTCTCGAGATCTGAAGACAGCCATAGAGAAAATTACTCAGAGAGGAGGACTTCTAAT  
GTAGGTGGGCCATCTCTTGTGACCAAGAACCTTCTTCCAAAGCCAATGAAACAGAACCGG  
GGCTCCCAATGTGGTGGTGGTGTGGATGGCTGGCCACGGACAAAGTGGAGGGAGCTTCAA  
GACTTGGAGAGAGTCAGGAATCACATTCTTCATCACCATTGAGGTGCTGCTGAAATGAG  
AAGCAGTATGTGGTGGAGGCCAACATTGCAAAACAGGCCCTCTACTC  
GCTCCACGTGAGAGCTGGTTGGCCTCCAAAGAACCTGGCCTGACATTGGCTTCGTACATGAC  
ACACTGACCGCCTGGCTGAGCAAGACCTGCTTGAACCTGGCTGACATTGGCTTCGTACATGAC  
GGCTCCAGCAGTGTGGGGACGGGCAACTTCCGACCGTCTCCAGTTGTGACAAACAGGCC  
AGAGTTTGAGATTCCGACACGGACACGCGCATCGGGGGCGTGCAGTACACCTACGAACAGGGC  
TGGAGTTGGTTCGACAAGTACAGCAGCAAGCCTGACATCCTCAACGCCATCAAGGGTGGC  
TACTGGAGTGGTGGCACCGAGCACGGGGCTGCCATCAACTTGCCTGGAGCAGCTCTCAAGAA  
GTCCAAGCCCAACAAAGAGGAAGTTAATGATCCTCATCAGCAGGGAGTCTACGACGAGTCC  
GGATCCAGCCATGGCTGCCATCTGAAGGGAGTGTACACCTATGCGATAGGCGTGTGGCTGGGCT  
GCCCAAGAGGGACTAGAAGTCACTGCCACTACCCCGCAGAGACCAACTCCTTGTGGACGA  
GTTTGACAAACCTCCATCAGTATGTCCTCAGGATCATCCAGAACATTGTTACAGAGTCAACTCAC  
AGCCTCGGAACTGAAATTCAAGAGCAGGAGCAGACAGCAAGTGTGCTTTACTAACTGACGTGTT  
GGACCACCCCCACCGCTTAATGGGGCAGCGACGGTGCATCAAGTCTGGCAGGGCATGGAGAAA  
AAATGTCCTGTTATTCTTGCATCATGCTTTTCAATTCCAAAACCTGGAGTTACAAAGA  
TGATCACAACGTATAGAATGAGCCAAAGGCTACATCATGTTGAGGGTGTGGAGATTTCACAT  
TTTGACAATTGTTCTAAAATAATGTTGGAATACAGTGCAGCCCTTACGACAGGCTTACGTTAG  
AGCTTTGTGAGATTGTTAAGTGTATTCTGATTTGAACTCTGTAACCCCTCAGCAAGTTCT  
TTTGTGTCATGACAATGAGGAATTGCTGAAATTAAATGTTAGAAGGGATGAAAAA  
AA  
AAG

## **FIGURE 34**

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKCPAG  
CQDPKYHVGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSLSLPRWR  
ESFIVLESKPKKGVTYPSALTYSSSKPAAQAGETTKAYQRPIP GTTAQPVTLMQLLAVTVAVA  
TPPTLPRPSPSAASTTSIPRQSVGHRSQEMDLWSTATYTSSQNRPRADPGIQRQDPSGAAFQKP  
VGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLFLIDGSTSIGKRRFRIQKQLLADVAQALDI  
GPAGPLMGVVQYGDNPATHFNLKHTNSRDLKTAIEKITQRGGLSNVGRAISFVTKNFFSKANGN  
RSGAPNVVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAENEKQYVVEPNFANKAVCRTNG  
FYSLHVQSWFGLHKTLOQPLVKRVCCTDRILACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTN  
LTKEFEISDTRIGAVQYTYEQRLEFGFDKYSSKPDILNAIKRVGWWSGGTSTGAAINFALQL  
FKKS KPNKRKLMILITDGRSYDDVRI PAMA AHLKGVITYAIGVAWAQEELEVIATHPARDHSFF  
VDEF DNLHQYVPRII QNICTEFNSQPRN

**Important features:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 181-200

**N-glycosylation sites.**

amino acids 390-394, 520-524

**N-myristoylation sites.**

amino acids 23-29, 93-99, 115-121, 262-268, 367-373, 389-395,  
431-437, 466-472, 509-515, 570-576, 571-577, 575-581, 627-633

**Amidation site.**

amino acids 304-308

## **FIGURE 35**

CCGAGCACAGGAGATTGCCTGCCTTAGGAGGTGGCTGCCTGTGGAAAAGCTATCAAGGAAGAAATTGC  
CAAACCATGCTTTTTCTGTTTCAGAGTAGTTACAACAGATCTGAGTGTAACTTAAAGCATGGAAT  
ACAGAAAACAACAAAAACTTAAGCTTAATTCTCATCTGGAATTCCACAGTTCTTAGCTCCCTGGACCC  
GGTTGACCTGTTGGCTCTCCCGCTGGCTGCTCTACACGTGGTGCTCTCGACTACTCACCCCGAGTGT  
AAGAACCTTCGGCTCGCGTCTGAGCTGCTGTGGATGGCCTCGGCTCTGGACTGTCCCTCCGAGTA  
GGATGTCACTGAGATCCCTCAAATGGAGCCTCTGCTGTCAGTCCTGAGTTCTTGATGTGGTAC  
CTCAGCCTCCCCACTACAATGTGATAGAACCGGTGAACGGATGTACTCTATGAGTATGAGCCGATT  
CAGACAAGACTTCACTCACACTCGAGAGCATTCAAACAGTCTCATCAAATCCATTCTGGTCATT  
TGGTGACCTCCCAACCCCTCAGATGAAAGCCAGGCCATTAGAGTTACTTGGGGTGAAGAAAGTCT  
TGGTGGGGATATGAGGTTCTACATTTCTTATTAGGCCAAGAGGCTGAAAGGAAGACAAATGTTGGC  
ATTGTCCTTAGAGGATGAAACACCTCTTATGGTACATAATCCGACAAGATTAGACACATATAATA  
ACCTGACCTTGAAACACCATTATGCCATTCAAGGGTAACTGAGTTTGCCCAATGCCAAGTACGTAATG  
AAGACAGACACTGATGTTCATCAAACTGGCAATTAGTGAAGTATCTTAAACCTAAACCACTCAGA  
GAAGTTTTCACAGGTTATCCTCTAAATTGATAATTATTCTATAGAGGATTACCAAAACCCATATT  
CTTACCAAGGAGTATCCTTCAAGGGTCCCTCCACTGCAGTGGGTTGGGTTATATAATGTCAGAGAT  
TTGGTGCCAAAGGATCTATGAAATGATGGTCACGTAAACCCATCAAGTTGAAGATGTTATGTCGGGAT  
CTGTTGAATTATTAAGTGAACATTCAATTCCAGAACACAAATTTCTTCTATAGATCC  
ATTGGATGTCCTGCAACTGAGACGTGTATTGCAGGCCATGGTTCTTCTTCAAGGAGATCATCACTTT  
TGGCAGGTATGCTAAGGAACACCAATGCCATTAAACTCACATTCTACAAAAGCCTAGAAGGACAG  
GATACCTTGAAAGTGTAAATAAGTAGGACTGTGGAAAATTCTATGGGAGGTCAGTGTGCTGGCTT  
ACACTGAACTCATGAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTTATTAGTCAGG  
CCCTCAAAGATGATATGTGGAGGAATTAAATATAAGGAATTGGAGGTTTGCTAAAGAAATTAGG  
ACCAAAACAATTGGACATGCTTGTAGACTAGAATTCTAAAAGGGTAACTGAGTTAAAGCTCA  
CTAGGCTGAAAAACAAACAAATGAGTTTATTGAAACAATGAGTCACTGAAAGGTTTGTA  
TATCTTATGTGGATTACCAATTAAAAATATATGAGTTCTGTGTCAAAAAAACTCTTCACTGAAGTTATA  
CTGAACAAAATTTCACCTGTTTGTCATTATAAGTACTTCAGATGTTGCTGAGTATTCACTGAGTTATT  
ATTATTAAATTACTTCACCTTGTGTTTAAATGTTTGACGATTCAACAGATAAAAGGATAG  
TGAATCATTCTTACATGCAAACATTCCAGTTACTTAACAGTCAAGTTATTGATAACATCACTCCA  
TTAATGAAAGTCATAGGTCAATTGCAATACAGTAATCTTGGACTTGTAAATATTACTGTGGT  
AATATAGAGAAGAATTAAAGCAAGAAAATCTGAAAA

## FIGURE 36

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPIYRQDFHF  
TLREHSNCNSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSSWWGYEVLTFFLLGQEAEKEDKMLA  
LSLEDEHLLYGDIIRQDFLDTYNNLTLKTIMAFRWVTEFCPNAKYVMKTDTDVFINTGNLVKYLL  
NLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPPFKVFPYCSCGLGYIMSRDLVPRIYEMMGHV  
KPIKFEDVYVGICLNLLKVNIIHPIPEDTNLFFLYRIHLDVCQLRRVIAAHGFSSKEIITFWQVMLR  
NTTCHY

**Important features:**

**Type II transmembrane domain:**

amino acids 20-39

**N-glycosylation sites.**

amino acids 72-76, 154-158, 198-202, 212-216, 326-330

**Glycosaminoglycan attachment site.**

amino acids 239-243

**Ly-6 / u-PAR domain proteins.**

amino acids 23-37

**N-myristoylation site.**

amino acids 271-277

## **FIGURE 37**

CGCTCGGGCACCGCCGGCAAGGATGGAGCTGGGTTGCTGGACGCAGTTGGGCTCACTTTCTCAGCTCCTCTCATC  
TCGTCCTGCCAAGAGACTACACAGTCATTAATGAAGCTGCCCTGGAGCAGAGTGGATAATCATGTCGGAGTGCCTGTG  
AATATGATCAGATTGAGTGCCTGCCCTGATCCACCCAGGTTGACCATCTTGAAGAAACTGCAAGAGCTGCCGAAATGGCTCATGGGGGGT  
TGAGTGTGACTCTGCCCTGATCCACCCAGGTTGACCATCTTGAAGAAACTGCAAGAGCTGCCGAAATGGCTCATGGGGGGT  
ACCTTGGATGACTCTATGTGAAGGGTTCTACTGTGCAGAGTGCCTGGAGGAGACTGCATGCGATGTG  
GCCAGGTTCTGCCAGGCCAAAGGGTCAGAGTTGTTGAAAGCTATCCCTAAATGCTCACTGTGAATGGACCATTCATGC  
TAAACCTGGGTTGTCACTCAACTAAGATTGTATGTGAGTCTGGAGTTGACTACATGTGCCAGTATGACTATGTGAG  
GTTCGTGATGGAGACAACCGCATGCCAGATCATCAAGCGTGTCTGTGCAACGAGCCAGCTCCATCCAGAGCATAG  
GATCCTCACTCCACGTCCTCTCCACTCCGATGCCAAGAATTGACGGTTCCATGCCATTATGAGGAGATCACAGC  
ATGCTCCTCATCCCTGTTCCATGACGGCACGTCCTGACAGGCTGGATCTACAGTGTCCCTGCTTGGCAGG  
TATACTGGGCAGCGCTGTGAAAATCTCCCTGAAGAAAGAAAAGTCTCAGACCCCTGGGGCCAGTCATGGTACCAAGAGAAA  
TAACAGGGGGCCCTGGGTTATCAACGGACGCCATGCTAAATTGGCACCGTGGTGTCTTCTTGTAAACAACCTCATGT  
TCTTAGTGGCAATGAGAAAAAGAATTGCGCAGCAGAATGGAGAGTGGTCAGGGAAACAGCCCATCTGCATAAAAGCCTGCCGA  
GAACCAAAGATTTCAGACCTGGTGAGAAGGAGAGTCTCCGATGCCAGGTTGACTCAAGGGAGACACCAATTACACCAGCTAT  
ACTCAGGCCCTTCAGCAAGCAGAAACTGCAGAGTGCCTTACCAAGAAGCCAGCCCTCCCTGGAGATCTGCCATGG  
ATACCAACATCTGCATACCCAGCTCCACTATGATGCATCTCACCCCTTACCCCGCTGGCAGCAGCAGGAGACATGT  
CTGAGGACTGGGAAGTGGAGTGGCGGGCACCATCCTGCATCCCTATGCGGGAAAATTGAGAACATCACTGCTCCAAAGA  
CCCAAGGGTTGCGCTGGCGTGGCAGGCCATCTACAGGAGGACAGCGGGTGCATGACGGCAGCCATACAAGGGAGC  
GTGGTTCTAGTGTGCGAGCGGTGCCCTGGTGAATGAGCGCAGTGTGGTGGCTGCCACTGTGTTACTGACCTGGGAAG  
GTCACCATGATCAAGACAGCAGACCTGAAAGTTGGGAAATTCTACCGGGATGATGACGGGATGAGAACAGCCATCC  
AGAGCCTACAGATTCTGCTATCATTGCACTCCAACTATGACCCCATCTGCTGATGACATGCCATCTGAAGCT  
CCTAGACAAGGCCGTATCAGCACCCAGTCCAGCCATCTGCCTCGCTGCCAGTCGGGATCTCAGCACTCCCTCAGGAG  
TCCCACATCACTGTGGCTGGCTGGAATGCTGCAGACGTGAGGAGCCCTGGCTTCAAGAACGACACACTGCCCTGG  
TGGTCAGTGTGGTGACTCGCTGCTGTGAGGAGCAGCATGAGGACCATGGCATCCAGTGTGACTGTGATAACATGTT  
CTGTGCCAGTGGGAAACCCACTGCCCTCTGATATCTGCACTGCAGAGACAGGAGGATCGCGCTGTGCTTCCCGGG  
CGAGCATCTCTGAGCCAGCGTGGCATCTGATGGGACTGGTCAGCTGGAGCTATGATAAAACATGCAGCCACAGGCTCTCCA  
CTGCCCTCACCAAGGTGCTGCCCTTAAAGACTGGATTGAAAGAAATGAAATGAACCATGCTCATGCACACTCCTGAGAAG  
TGTGTTCTGATATCGCTGTACGTGTGTCATTGCGTAAGCAGTGTGGGCTGAGTGTGATTTGGGCTGTGAACTGGCT  
GTGCCAGGGCTCTGACTTCAGGGACAAAACCTCAGTGAAGGGTGAAGTAGACCTCATTGCTGGTAGGCTGATGCCGCTCCA  
CTACTAGGACAGCCAATTGGAAGATGCCAGGGCTTGCAAGAAGCTAAGTTCTCAAAAGAACGACCATATACAAAACCTCTCCA  
CTCCACTGACCTGGGGCTTCCCAACTTCAGTATGCAATGCCATCAGCTTGACCCAGGGAAAGATCTGGGCTCATGAG  
GCCCTTGGAGGCTCTCAAGTTCTAGAGAGCAGCTGCCCTGGGACAGCCAGGGCAGCAGAGCAGCTGGGATGTGGTGCATGCC  
TGTGTACATGCCACAGTACAGTCTGGCTTCTCCCTCCATCTCTGATACACATTAAATAAGGGTTGGCTCT  
GAAACTACAA  
AA

## FIGURE 38

MELGCWTQLGLTFLOLLLISSLPREYTVINEACPGAEWNIMCRECCYEYDQIECVCPGKREVVGYT  
IPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGTLDDFYVKGFYCAECRAGWYGGDCMRCGQ  
VLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDQII  
KRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSPCFHDTGCVLDKAGSYKC  
ACLAGYTQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTVVSFFCNNSYVLSNE  
KRTCQQNGEWSGKQPIKACREP KISDLVRRRVLPMQVSRETPLHQLYSAAFSKQKLQSAPTK  
KPALPFGDLPGMYQHLHTQLQYECISPFYRRLGSSRTCLRTGKWSGRAPSCIPI CGKIENITAP  
KTQGLRWPWQAAIYRRRTSGVHDGSLHKGAWFLVCS GALVNERTVVVAHCVTDLGKVTMIKTADL  
KVVLGKFYRDDDREKTIQSLQISAIILHPNYDPILL DADIAILKLLDKARISTRVQPI CLAASR  
DLSTS FQESHITVAGWNVLADVRSPGFKN DTLRSGVVSVVDSLLCEEQHEDH GIPVS VTDNMFCA  
SWEPTAPS DICTAETGGIAAVSF PGRASPEPRW HLMGLVWSYDKTCSHRLSTAFTKVL PFKDWI  
ERNMK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-23

**EGF-like domain cysteine pattern signature.**

amino acids 260-272

**N-glycosylation sites.**

amino acids 96-100, 279-283, 316-320, 451-455, 614-618

**N-myristylation sites.**

amino acids 35-41, 97-103, 256-262, 284-290, 298-304, 308-314,  
474-480, 491-497, 638-644, 666-672

**Amidation site.**

amino acids 56-60

**Serine proteases, trypsin family.**

amino acids 489-506

**CUB domain proteins profile.**

amino acids 150-167

## **FIGURE 39**

GTGTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTCTTACGGGCCGTGATTTATAACGTGGCTTAATC  
TGAAGGTTCTCAGTCATAATTCTTGTGATCTACTGATTGTGGGGCATGCCAAGGTTGCTTAAGGAGCTTGGCTGG  
TTTGGGCCCTGTAGCTGACAGAAGGTGCCAGGGAGAATGCAGCACACTGCTGGAGAATGAAGGCCTCTGTTGC  
TGGCTTGCTTGGCTCAGTCCTGCTAATCATTGACAATGTGGCAACTGCACTTCCTGTATTCAAGACTCTGTA  
AAGGTGCCCTCCACTACGGCCTGACCAAGAATAGGAAGGGCGTCACAAGATGGCTGTCAGACGGCTGCGAGCC  
TCACAGGCCAGGCTCCCTCCCCAGAGGTTCTGCAGTGCCACCATCTCTTAATGACAGACGAGGCTGGCTAGACA  
ACCCCTGCCATCGTGTCTGGCAGAGGACGGCAGCCAGCAATCAGCCAGTGGACTCTGGCCGGAGCAACCGAACTA  
GGGCACGGCCCTTGAGAGATCCACTATTAGAAGCAGATCATTAAAAAAATAATCGAGCTTGAGTGTCTTCGAA  
GGACAAAGAGCGGGAGTGCAGTTGCAACCATGCCGACCAGGGAGGAAATTCTGAAAACACCAGTGCCTGAGA  
TCTTCTCAAGGTTGTAACACCTGATTCCAGATGGTGAATTACAGCATCAAGATCAATCGAGTAGATCCAGTGA  
GCCCTCTATTAGGCTGGGGAGGTAGCGAAACCCACTGGTCATATCATTATCAAACACATTATCGTATGGGG  
TGATCGCCAGAGACGGCCGGCTACTGCCAGGAGACATCATTCTAAAGGTCAACGGATGGACATCAGCAATGTCCTC  
ACAACACTACGCTGTGCGTCTCTGCCAGGCTGCCAGGTGCTGCTGACTGTGATGCGTGAACAGAATTCGCGA  
GCAGGAACAATGGACAGGCCCGATGCCATCAGACCCAGATGACAGCTTCATGTGATTCTCAACAAAAGTAGCC  
CCGAGGAGCAGCTTGGATAAAAATGGTGCAGAAGGTGGATGAGCTGGGTTTCATCTCAATGTGCTGGATGGCG  
GTGTCATATCGACATGGTCAGCTTGAGGAGAATGACCGTGTGTTAGCCATCAATGGACATGATCTCGATATGGCA  
GCCAGAAACTGCCAGGGGGAGCATCACATAGAGAATGGGATTTGCCATCTATGTCATCAGTGTGAGCCGGAGGG  
GGAGCCCTGACATCTTCAGGAAGCCGGCTGAAACAGCAATGGCAGCTGGTCCCAGGGCCAGGGAGAGGAGCAACA  
CTCCCAAGCCCTCCATCTACAATTACTGTCATGAGAAGGTGTTAAATCTCAAAAGACCCGGTGAATCTCTCG  
GCATGACCGTGCAGGGGGAGCATCACATAGAGAATGGGATTTGCCATCTATGTCATCAGTGTGAGCCGGAGGG  
TCATAAGCAGAGATGGAAGAATAAAAACAGGTGACATTGTTGAATGTGGATGGGTCGAACGTGACAGAGTCAGCC  
GGAGTGAGGCACTGGCATTATTGAAAAAGAACATCATCTCGATGACTACTCAAAGCTTGGAAAGTCAAAGAGTATGAGC  
CCCAGGAAGACTGCAGCAGGCCAGCAGCCCTGGACTCAACACATGGCCCAACCCAGTGAATGGTCCCCATCTC  
GGGTATGTGGCTGAAATTACCCAGGTGCTGTATAACTGTAAGAGATATTGTTACAGAAGAAACACAGCTGGAAAGTC  
TGGGCTCTGCAATTGAGGTTATGAGAAGAACATGAAACAAACCTTTTCATCAAATCATTGTTGAAGGAA  
CACAGCATAATGATGGAAGAATTAGATGTGGTGAATTCTCTGCTGCAATGGTAGAAGTACATCAGGAATG  
TACATGCTGCTGGCAAGACTGCTGAAAGAACATTAAAGGAGAACATTACTCTAACATTGTTCTGGCTGGCACTT  
TTTATAGAATCAATGATGGTCAGAGGAAACAGAAAAATCACAAATAGGCTAAGAAGTGAACACTATATTATC  
TTGTCAGTTTATATTAAAGAAGAACATTGTAAGGAAAGTATGTCAGGAAAGTATGATCATCTAATGAAAGCCAGTT  
ACACCTCAGAAATATGATCCAAAAAAATTAAACTACTAGTTTTTCAGTGTGGAGGATTCTCATTACTCTAC  
AACATTGTTTATATTCTATTCAATAAAAAGCCCTAAACAACTAAATGATTGATTGTTGATACCCACTGAATT  
CAAGCTGATTAAATTAAATTGGTATATGCTGAGTCTGCCAAGGGTACATTATGCCATTAACTTACAGCT  
AAAATTTTAAATGCTGAGAACCTGGTCTGTTCATCAAACAAAGAATAAATTTTACAGTTAA

## **FIGURE 40**

MKALLLLVLPWLS PANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPDCASLTATAPS  
PEVSAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDGRSNRTRARPFERSTIRSRSFKKINR  
ALSVLRRTKSGSAVANHADQGRENSENTTAPEVFPRLYHLLPDGEITSIKINRVDPSESLSIRLV  
GGSETPLVHIIIQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLLRQPCQVLWLTVM  
REQKFRSRNNGQAPDAYRPRDDS FHVLNKSSPEEQLGIKLVRVDEPGVFI FNVLDGGVAYRHG  
QLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVSRQVRQSPDIFQEAGWNSNGSWSPG  
PGERSNTPKPLHPTITCHEKVNNIQKDPGESLGMTVAGGASHREWDLPIYVISVEPGGVISRDGR  
IKTGDILLNVDGVELTEVSREAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNHNMAPP  
SDWSPSWVMWLELPRLYNCKDIVLRRNTAGSLGFCIVGGYEEYNGNKPFFIKSIVEGTPAYNDG  
RIRCGDILLAVNGRSTSGMIHACLRLLKELKGRITLTIVSWPGTFL

**Important features:**

**Signal peptide:**

amino acids 1-15

**N-glycosylation sites.**

amino acids 108-112, 157-161, 289-293, 384-388

**Tyrosine kinase phosphorylation sites.**

amino acids 433-441, 492-500

**N-myristoylation sites.**

amino acids 51-57, 141-147, 233-239, 344-350, 423-429, 447-453,  
467-473, 603-609

## **FIGURE 41**

ACCAGGCATTGTATCTCAGTTGTCATCAAGTCGCAATCAGATTGGAAAAGCTCAACTGAAAGCTT  
CTTGCCTGCAGTGAAGCAGAGAGATAGATATTACACGTAATAAAAAACATGGGCTCAACCTGACT  
TTCCACCTTCCTACAAATTCCGATTACTGTTGCTGACTTTGTGCTGACAGTGGTTGGGGC  
CACCAGTAACTACTCGTGGGTGCCATTCAAGAGATTCTAAAGCAAAGGAGTTCATGGCTAATTCC  
ATAAGACCCCTATTGGGAAGGGAAAAACTCTGACTAATGAAGCATTCCACGAAGAAGGTAGAACTT  
GACAACGTCCCTCTGTCTCCTTACCTCAGAGGCCAGAGCAAGCTATTCAAACCAAGATCTCAC  
TTTGGAAAGAGGTACAGGCAGAAAATCCAAAGTGTCCAGAGGCCGGTATGCCCTCAGGAATGTAAG  
CTTACAGAGGGTCGCCATCCTCGTCCCCACCGGAACAGAGAGAAAACACCTGATGTACCTGCTGGAA  
CATCTGCATCCCTCCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTATCCACCAGGCTGAAGG  
TAAAAGTTAATCGAGCCAAACTCTTGAATGTGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGG  
ACTGCTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTACAAGTGTGAGGAG  
CATCCCAAGCATTGGTGGTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTGGATATTGG  
GGGTGTACTGCCCTAACAGCAGAGGAGCAGTTCAAGGTGAATGGATTCTCTAACAAACTACTGGGAT  
GGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAGAATGAAAATTCCGGCCCTG  
CCTGAAGTGGTAAATATACAATGGTCTTCCACACTAGAGACAAAGGCAATGAGGTGAACCGAGAACG  
GATGAAGCTCTTACACCAAGTGTACAGAGTCTGGAGAACAGATGGGTGAGTAGTTGTTCTTATAAT  
TAGTATCTGTGGAACACAATCCTTATATATCAACATCACAGTGGATTCTGGTTGGTGCATGACCC  
TGGATCTTGGTGAATGGAAAGAAGTATTCTTGTGCAATAATTGGCTAGAGACTCAA  
ATAGTAGCACACATTAAGAACCTGTTACAGCTCATGGTGAAGCTGAATTTCCTTTGTATTCT  
TAGCAGAGCTCTGGTGAATGGAAAGTATTCTTGTGCAATAATTGGCTAGAGACTCAA  
CATGAGGGTTAAATATTGTAATATGGATACTGAAAGGACTTTATATAAAAGGATGACTCAAAGGATAA  
AATGAACGCTATTGAGGACTCTGGTGAAGGAGATTATTAAATTGAAAGTAATATATTATGGGAT  
AAAAGGCCACAGGAAATAAGACTGCTGAATGTCAGAGAGAACCCAGAGTTCTCGTCCAAGGTAGAA  
AGGTACGAAGATAACAATACTGTTATTCAATTCTGTACAATCATCTGTGAAGTGGTGGTGTCAAGT  
GAGAAGGCCTCACAAAGAGGGAGAAAAGGCAGCAATCAGGACACAGTGAACCTGGGAATGAAGA  
GGTAGCAGGAGGGTGGAGTGTCCGCTGCAAAGGCAGCAGTAGCTGAGCTGGTTGCAGGTGCTGATAGC  
CTTCAGGGGAGGACCTGCCAGGTATGCCTCCAGTGATGCCACCAGAGAATACATTCTATTAGT  
TTTAAAGAGTTTGAAATGTTGACAAGTAGGATATGAATTAGCAGTTACAAGTTACAT  
ATTAACATAATAATGTCTATCAAACCTCTGTAGTAAATGTGAAAAGCAAA

## **FIGURE 42**

MGFNLTFHLSYKFRLLLLLTLCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLLIGKGKTLTN  
EASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRVAILVPH  
RNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEENWDCFI FHDV  
DLVPENDFNLYKCEEHPKHLVGRNSTGYRLRYSGYFGGVTAALSREQFFKVNGFSNNYWGWGGED  
DDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSRVWRTDGLSSCSYKLV  
SVEHNPLYINITVDFWFGA

**Important features:**

**Signal peptide:**

amino acids 1-27

**N-glycosylation sites.**

amino acids 4-8, 220-224, 335-339

**Xylose isomerase proteins.**

amino acids 191-202

### **FIGURE 43**

## **FIGURE 44**

MALSSQIWAACLLLLLLASLTGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRDTHFPI  
CIFCCGCCHRSKCGMCCKT

**Important features:**

**Signal peptide:**

amino acids 1-24

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 58-59

**N-myristoylation site.**

amino acids 44-50

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 1-12

## **FIGURE 45**

GTGGCTTCATTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCACCC  
TCATCTATATCCTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTGGTCGGT  
TCCGTTGGTGGGCGGTGACTTCCCCCTGAAGTCAAAGTAAAGCAAGTTGACTCTATTGTCTG  
GACCTTCAACACAACCCCTCTTGTACCACAGCCAGAAGGGGGCACTATCATAGTGACCCAAA  
ATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAGCTCAGCAAACGTAAAG  
AAGAATGACTCAGGGATCTACTATGTGGGATATACAGCTCATCAGCAGCCCTCCACCCA  
GGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCTAAAGTCACCATGGGTCTGCAGAGCA  
ATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGAAGAGGATGTGATT  
TATACTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTC  
CTGGAGATGGGGAGAAAGTGAATATGACCTTCATCTGCCTGCCAGGAACCTGTCAAGCAGAACT  
TCTCAAGCCCCATCCTGCCAGGAAGCTGTGAAGGTGCTGCTGATGACCCAGATTCCCTCCATG  
GTCCTCCTGTGTCTCCTGTTGGTGCCTCCTGCTCAGTCCTTGACTGGGCTATTCTTG  
GTTTCTGAAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGTGGACATTGTCGGG  
AAACTCCTAACATATGCCCTATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAAT  
AGAACAAATCCTAAAGGAAGATCCAGCAAATACGGTTACTCCACTGTGAAATACGAAAAAGAT  
GGAAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTGCCTATGAGAATGTTA  
TCTAGACAGCAGTGCACTCCCCTAAGTCTGCTCA

## **FIGURE 46**

MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLSKVKQVDSIVWTFTNTPLVTIQP  
EGGTIIVTQNRNRERVDFPDGGYSLKLSKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLSK  
PKVTMGLQSNKNGTCVTNLTCMEHGEEDVIYTWKALGQAANESHNGSILPISWRWGESDMTFIC  
VARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLVPLLLSPVLGLFLWFLKRERQEEYIE  
EKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPANTVYSTVEIPKKMENPHSLLTMPDT  
PRLFAYENVI

**Important features:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 224-250

**Leucine zipper pattern.**

amino acids 229-251

**N-glycosylation sites.**

amino acids 98-102, 142-146, 148-152, 172-176, 176-180, 204-208,  
291-295

## **FIGURE 47**

GGCTCGAGCGTTCTGAGCCAGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAATGG  
ATTCAGCCCTGCTGGTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTGTCAGCT  
TAGTTGAGGAAGACCAATTTCCAAAACCCCATCTCTGCTTGAGTGGTGGTCCCAGGAATT  
ATAGGAGCAGGTCTGATGCCATTCCAGCAACAACAATGTCCTTGACAGCAAGAAAAAGAGCGTG  
CTGCAACAACAGAACTGGAATGTTCTTCATCATTTCAGTCAGTGTGATCACAGTCATTGGTGCTC  
TGTATTGCATGCTGATATCCATCCAGGCTCTCTAAAGGTCCCTCATGTAATTCTCCAAGC  
AACAGTAATGCCAATTGTAATTTCATTGAAAAACATCAGTGACATTCCAGAACATCCTCAA  
CTTGCAGGTGGTTTCAATGACTCTTGCACCTCCTACTGGTTCAATAAACCCACCAGTAACG  
ACACCATGGCGAGTGGCTGGAGAGCATCTAGTTCCACTTCGATTCTGAAAGAAAACAAACATAGG  
CTTATCCACTCTCAGTATTTAGGTCTATTGCTTGGAAATTCTGGAGGTCCTTGGGCT  
CAGTCAGATAGTCATCGGTTCCGGCTGTCGTGGAGTCTAAGCGAAGAAGTCAAATTG  
TGTAGTTAATGGGAAAAAATGTAAGTATCAGTAGTTGAAAAAAA

## **FIGURE 48**

MTCCEGWTSCNGFSLLVLLLGVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPA  
TTMSLTARKRACCNNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPSNSNANCEFSL  
KNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRLIHFSVFLGL  
LLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

**Important features:**

**Transmembrane domains:**

amino acids 10-31 (type II), 50-72, 87-110, 191-213

**N-glycosylation sites.**

amino acids 80-84, 132-136, 148-152, 163-167

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 223-227

**N-myristylation sites.**

amino acids 22-28, 54-60, 83-89, 97-103, 216-222

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 207-218

**TNFR/NGFR family cysteine-rich region protein.**

amino acids 4-12

## **FIGURE 49**

ATCCGTTCTGCGCTGCCAGCTCAGGTGAGCCCTGCCAAGGTGACCTCGCAGGACACTGGTGA  
AGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTGGAGCAG  
ATCCGTGGGCTGCAGACCCCCCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCTGAACTGTGA  
CATGGAGAGAGTGACCTGGCCCTTCCTACTGGCAGGCCTGACTGCCTTGGAAAGCCAATGACC  
CATTTGCCAATAAGACGATCCCTCTACTATGACTGGAAAAACCTGCAGCTGAGCGGACTGATC  
TGCAGGGCTCCTGCCATTGCTGGATCGCGCAGTCTGAGTGGCAAATGAAATACAAGAG  
CAGCCAGAACGAGCACAGTCCTGTACCTGAGAAGGCCATCCACTCATCACTCCAGGCTCTGCCA  
CTACTTGCTGAGCACAGGACTGGCCTCCAGGGATGGCCTGAAGCCTAACACTGCCCTCAGCACC  
TCCTCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTCTCTCCAAGGGCAGGCTGTTAGGCCCT  
TTCTGATCAGGAGGCTTCTTATGAATTAAACTGCCACCACCCCTCA

## **FIGURE 50**

MERVTLALLLLAGLTALLEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKYKS  
SQKQHSPVPEKAIPPLITPGSATT

**Important features:**

**Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 36-59

**N-myristoylation sites.**

amino acids 41-47, 45-51, 84-90

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7.**

amino acids 54-67

## **FIGURE 51**

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGAGGG  
AGGACAGGGAGTCGGAAGGAGGAGCACAGAGGAGGGCACAGAGACCCAGAGCAAGGGCGGCAAGG  
AGGAGACCCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGCTGGCAGAGATGAAGTCCAG  
GGGCCCCCTGGCCTGCCCTGCTGGCCCTGCGCTGGCAGTGGGAGGCTGGCCCTGAG  
CGGAGAGGAAAGCACTGGACAAATATTGGGAGGCCCTGGACATGGCCTGGAGACGCCCTGA  
GCGAAGGGTGGAAAGGCCATTGGCAAAGAGGCCGGAGGGCAGTGGCTCTAAAGTCAGTGAG  
GCCCTGGCCAAGGGACCAGAGAACAGCTGGCACTGGAGTCAGGCAGGTTCCAGGCTTGGC  
AGCAGATGCTTGGCAACAGGGTCGGGAAGCAGCCATGCTCTGGAAACACTGGCAGGAGA  
TTGGCAGACAGGCAGAACAGATGTCATTGACACGGAGCAGATGCTGTCGCGGCTCCTGGCAGGG  
GTGCCTGGCCACAGTGGTGGCTGGAAACTCTGGAGGCCATGGCATCTTGGCTCTCAAGGTGG  
CCTTGGAGGCCAGGGCCAGGGCAATCCTGGAGGTCTGGGACTCCGTGGTCCACGGATACCCCG  
GAAACTCAGCAGGCAGCTTGGAAATGAATCCTCAGGGAGCTCCCTGGGTCAAGGAGGCAATGG  
GGGCCACCAAACCTTGGGACCAACACTCAGGGAGCTGTGGCCAGCAGCTGGCTATGGTCAGTGAG  
AGCCAGCAACCAGAACATGAAGGGTCACGAATCCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCA  
ACTCTGGGGAGGCAGCGGTCACAGTCGGCAGCAGTGGCAGTGGCAGCAATGGTACAACAAAC  
AATGGCAGCAGCAGTGGTGGCAGCAGCAGCAGTGGCAGCAGCAGCAGTGGCAGCAG  
TGGCGGCAGCAGTGGTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGAGTGA  
CCTCCTGGGATCCAGCACCGGCTCCTCCGGCAACCACGGTGGGAGCGGGAGGAAATGG  
CATAAACCCGGGTGTGAAAAGCCAGGGAAATGAAGCCCGGGAGCGGGGAATCTGGGATTCA  
CTTCAGAGGACAGGGAGTTCCAGCAACATGAGGGAAATAAGCAAAGAGGGCAATGCCCTT  
GAGGCTCTGGAGACAATTATCGGGGCAAGGGTCGAGCTGGGAGTGGAGGAGGTGACGCTGTT  
GGTGGAGTCATACTGTGAACCTCTGAGACGGCTCCTGGGATGTTAACCTTGACACTTCTGGAA  
GAATTTAAATCCAAGCTGGTTCATCAACTGGATGCCATAAACAGGACAGAGCTCTC  
GCATCCCGTGACCCTCCAGACAAGGAGCCACCAGATTGATGGAGCCCAACTCCCTCTTAA  
AACACCACCCCTCATCACTAATCTCAGCCCTGGCTTGAATAAACCTTAGCTGCCCAACAAA  
AA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 52**

MKFQGPLACLLLALCLGSGEAGPLQSGEESTGNTIGEALGHGLDALSEGVGKAIGKEAGGAAGSKVS  
EALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHGADAVRGSWQGVP  
GHSGAWETSGGHGIFGSQGGLGGQGQGNPGGLGTPWVHGYPGNSAGSFGMNPQGAPWGQGGNGPPNF  
GTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGSSNSGGSGSQSGSSGSGSNGDNNNGSSSGS  
SSGSSSSGSSGGSSGGSSGGSGNSGGSRGDGSESSWGSSTGSSSGNHGGSGGGNGHKPGCEKPGNE  
ARGSGESGIQGFRGQQGVSSNMREISKEGNRLGGSGDNYRGQGSSWGSGGDAVGGVNTVNSETS PGM  
FNFDTFWKNFKSKLGFINWDAINKDQRSSRIP

**Signal peptide:**

amino acids 1-21

**N-glycosylation site.**

amino acids 265-269

**Glycosaminoglycan attachment site.**

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

**Casein kinase II phosphorylation site.**

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

**N-myristoylation site.**

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80,  
90-96, 96-102, 130-136, 140-146, 149-155, 152-158, 155-161,  
159-165, 163-169, 178-184, 190-196, 194-200, 199-205, 218-224,  
236-242, 238-244, 239-245, 240-246, 245-251, 246-252, 249-252,  
253-259, 256-262, 266-272, 270-276, 271-277, 275-281, 279-285,  
283-289, 284-290, 287-293, 288-294, 291-297, 292-298, 295-301,  
298-304, 305-311, 311-317, 315-321, 319-325, 322-328, 323-329,  
325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389,  
387-393, 389-395, 395-401

**Cell attachment sequence.**

amino acids 301-304

## **FIGURE 53**

GGAGAAGAGGTTGTGAGGACAAGCTGCTCCGACAGAAGG**TG**CGCTGCTGAGCCTGCCCTGG  
CTGGGCCTCAGACCGGTGGCAATGTCCCCATGGCTACTCCTGCTGCTGGTTGAGGCTCCAGTGGCT  
ACTCGCCCGCATCCTGGCTTGGACCTATGCCCTATAACAACTGCCGCCGGCTCCAGTGGCT  
CACAGCCCCAAAACGGAACGGTTGGGTCACCTGGGCTGATCACTCCTACAGAGGAGGGC  
TTGAAGGACTCGACCCAGATGTCGGCCACCTATTCCAGGGCTTACGGTATGGCTGGGCTCCAT  
CATCCCCCTCATCGTTTATGCCACCCCTGACACCCTGGCTATCACCAATGCCCTAGCTGCCA  
TTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGGCTGGAGAAGGGATACTGCTG  
AGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGACGCCGCCCTCCATTCAACATCCT  
GAAGTCCTATATAACGATCTCAACAAGAGTGCAACATCATGCTTGACAAGTGGCAGCACCTGG  
CCTCAGAGGGCAGCAGTCGTCGGACATGTTGAGGACATCAGCCTCATGACCTGGACAGTCTA  
CAGAAATGCATCTTCAGCTTGACAGCCATTGTCAGGAGAGGCCAGTGAATATATTGCCACCAT  
CTTGGAGCTCAGTGCCCTGTAGAGAAAAGAAGCCAGCATACTCCAGCACATGGACTTCTGT  
ATTACCTCTCCCATGACGGCGCGCTTCCACAGGGCCTGCCGCTGGTCATGACTTCACAGAC  
GCTGTCATCCGGGAGCGCGTCGCACCCCTCCACTCAGGGTATTGATGATTTCAAAGACAA  
AGCCAAGTCCAAGAGACTTGGATTTCATTGATGTGCTTGCTGAGCAAGGATGAAGATGGAGG  
CATTGTCAGATGAGGATATAAGAGCAGAGGCTGACACCTTCATGTTGGAGGCCATGACACCACG  
GCCAGTGGCCTCTCCTGGGTCTGTACAACCTTGCAGGCACCCAGAAATCCAGGAGCGCTGCCG  
ACAGGAGGTGCAAGAGCTTCTGAAGGACCCGATCTAAAGAGATTGAATGGGACGACCTGGCCC  
AGCTGCCCTTCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATC  
TCCCAGTGCACCCAGGACATTGTTCTCCAGATGGCGAGTCATCCCCAAAGGCAATTACCTG  
CCTCATCGATATTATAGGGGTCATCACAAACCCAACTGTGTCGGCCGATCCTGAGGTCTACGACC  
CCTTCCGCTTGACCCAGAGAACAGCAAGGGAGGTCACTCTGGCTTATTCCCTTCTCCGCA  
GGGCCAGGAACATGCATGGGCAGGCAGTCGCATGGCGAGATGAAAGTGGCCTGGCGTTGAT  
GCTGCTGCACCTCCGGTCTGCCAGACCAACTGAGCCCCGCAGGAAGCTGGAATTGATCATGC  
GCGCCGAGGGCGGGCTTGGCTGCGGGTGGAGCCCTGAATGTAGGCTTGCA**G****T**ACTTCTGAC  
CCATCCACCTGTTTTGCAGATTGTCATGAATAAACGGTGCTGTCAAA

## **FIGURE 54**

MSLLSLPWGLRPVAMSPWLLLLVVGSWLLARILAWTYAFYNNCRLQCFPQPPKRNWFWGHLG  
LITPTEEGLKDSTQMSATYSQGFTVWLGPPIIPFIVLCHPDTIRSITNASAAIAPKDNLFIRFLKP  
WLGEGLLSSGGDKWSRHRMLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGSSRLDMFEHI  
SLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYYLSHDGRRFHRAC  
RLVHDFTDAVIRERRTLPTQGIDFFKDKAKSKTLDFIGVLLSKDEDGKALSDEDIRAEADTF  
MFGGHDTTASGLSWLYNLRHPEYQERCQEVAELLKDRDPKEIEWDDLAQLPFLTMCVKESLR  
LHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVWPDPPEVYDPFRDPENSKGRSP  
LAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHTEPRRKLEIMRAEGGLWLRVEPLN  
VGLQ

**Important features:**

**Transmembrane domains:**

amino acids 13-32 (type II), 77-102

**Cytochrome P450 cysteine heme-iron ligand signature.**

amino acids 461-471

**N-glycosylation sites.**

amino acids 112-116, 168-172

## **FIGURE 55**

ATCGCATCAATTGGGAGTACCATCTTCCTCATGGGACCAGTGAAACAGCTGAAGCGAATGTTGA  
GCCTACTCGTTGATTGCAACTATCATGGTGCTGTGTTGCACTTACCCGTGTTCTGCCT  
TTTGGTGGCATAACAAGGGACTTGCACTTATCTTCTGCATTTGCAGTCTTGCATTGACGTGG  
TACAGCCTTCCTTCATACCATTGCAAGGGATGCTGTGAAGAAGTGTGTTGCCGTGTCTGC  
ATAATTCATGCCAGTTTATGAAGCTTGAAGGCACTATGGACAGAAGCTGGGACAGTTT  
GTAACTATCTCGAAACCTCTGTCTTACAGACATGTGCCTTTATCTTGCAGTGTTGCTT  
GTGATTGAAACATTGAGGGTTACTTTGGAAGCAACAATACATTCTCGAACCTGAATGTCAGTA  
GCACAGGATGAGAAGTGGGTTCTGTATCTTGAGTGGAACTTCCTCATGTACTGTTCTC  
TCTGGATGTTGTCCCACTGAATTCCCATGAATAACAAACCTATTCAGCAACAGCAAAAAAAAAA  
AAA

## **FIGURE 56**

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCASFWWHNGLALIFCILOSLALTWYSLSFIPFAR  
DAVKKCFAVCLA

**Important features:**

**Signal peptide:**

amino acids 1-33

**Type II fibronectin collagen-binding domain protein.**

amino acids 30-72

## FIGURE 57

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGCAGTGGAGCACCCAGCAGGCCAACATGCTGTCTGTGCCCTG  
TACGTGCCGTCATCGGGGAAGCCCAGCCGAGTTCACTGACTTTGAGTCGAAGGGCTCCGCCAGCTGAAGTCC  
ATTTCAAGCTCAGTGTCTTCATCCCCCTCCAGGAATTCTCACCTACCGCCAGTGGAAAGCAGAAAATTGTACAAGCT  
GGAGATAAGGACCTTGATGGCAGCTAGACTTTGAAGAATTGTCCATTATCTCAAGATCATGAGAAGAAGCTGAGG  
CTGGTGTAAAGATTTGGACAAAAGAATGATGGACGCATTGACGCCAGGAGATCATGCAGTCCCTGCCGGACTTG  
GGAGTCAAGATATCTGACAGCAGGCCAGAAAATTCTCAAGAGCATGGATAAAAAGCCAGCATGCCATCGACTGG  
AACAGTGGAGAGACTACCACCTCCACCCCTGGAAACATCCCGAGATCATCCTACTTGAAGCATTCCACG  
ATCTTGATGTGGGTGAGAATCTAACGGTCCCGATGAGTTCACAGTGGAGGAGGGCAGACGGGGATGTGGTGGAGA  
CACCTGGTGGCAGGGAGTGGGGCAGGGCCGTATCCAGAACCTGCACGGCCCCCTGGACAGGCTCAAGGTCTCATG  
CAGGTCCATGCCCTCCCGCAGCAACATGGCATCTGGTGTGGCTCACTCAGATGATTGAGAAGGGAGGGCCAGG  
TCACTCTGGGGCAATGGCATCACCTCTCAAATTGCCCTGGCAGGATCATGCCATCAATTATGCCATGAGCAG  
ATCAAGGCCCTTGTGTAGTGACCAAGGAGACTCTGAGGATTCAAGAGAGGTTGGCAGGGTCTTGGCAGGGCC  
ATCCTCCAGAGCAGCATCACCAATGGAGGTCCTGAAGACCCGGATGGCCTGCCAGAACAGGCCAGTACTCAGGA  
ATGCTGGACTGCCCCAGGAGATCTGGCAGAGAGGGGTGGCCCTTCTAACAAAGGCTATGCCCCAACATGCTG  
GGCATCATCCCTATGCCGCATCAGCCATTGCACTGAGACGCTCAAGAATGCTGGCTGCAGCAGTATGCACTG  
AACAGCCGGACCCCGGGTGTGTGCTCTGGCCTGGCAGGATCTGGCAGGCTGGCCAGCTGGCCAGCTAC  
CCCCCTGGCCATGCAAGGACCCGGATGCAAGGCGAACGCTTATTGAGGGCGTCCGGAGGTGACCATGAGCAGCTC  
TTCAAAACATATCTGGGAGGAGGGGCTTCGGCTGTACAGGGGCTGGCCCAACTTCATGAAGGTATCCCC  
GCTGTGAGCATCAGCTACGTGGTCTACGAGAACCTGAAGATCACCTGGCGTGCAGTCGGGGTGACGGGGGGAGGGC  
CGCCCGGACTGGACTGGCTGATCCTGGCAGGCTACAGGAGGGCTACAGGAGGGCTACATTGTGAATGTGCCAACACT  
AAGCTGTCTCGAGGCAAGCTGTGAAAACCTAGACGCCACCCGAGGGGGAGGTGGAGAGCTGGCAGGCCAGGGCTT  
GTCTGTGAGCCAGACCCCTCTGTGGTCTGGCTCAAGCAAGACCAAGGGCTTCAAGGGTCCAGGGTACAGCAGG  
CTCCGGGCTCACATGTCAAGGACAGGACATTTCAGTGCAGTCCTGGCAATAGTGAAGCTGGAGGCTGGAGGCC  
TAGTTCTCCATTTCACCCCTGAGCAGCTGGCCACGGCCCTGCCCTGTGCTGCCGTCATCTCCCTGTG  
CCTCTGTGCTGCCCTGCTGCTGAGGTAAGGTGGAGGGAGGGCTACAGGCCAACATCCCACCCCTCGTCCAATCCC  
ATAATCCATGATGAAAGGTGAGGTGAGCTGGCCCTCCAGGCTGACTGGCTTCAAGGGCTTCAACAGCATTGAGC  
TGTGAAGGAAGGAAAGGATCTGGCTTCAAGGAGGGCTGGCTGACTGGCTTCAAGGGCTTCAAGGGCTTCAAGGG  
CTTGGGGAGTGCAGGGGCTGGCTGGCTGCACAGAAGGCAAGTGTGGGCTCATGGTCTGAGCT  
GGCCTGGACCCCTGTCAAGGATGGGCCACACTCAGAACCAAACACTCAGTGTCCCCACTGTGGCATGAGGCAAGTGGAGCA  
CCATTTTGAGGGCGAAGGGCAGAGCGTTCTGTGTTCTGGGAGGGAAAGGAAAGGTGTGGAGGGCTTAATTATGG  
ACTGTTGGGAAAGGGTTGGCTCAGGAGGACAGGAGGGCTGGGACTTGTGCTTCAAGGGCTTCAAGGGAGAGCAGG  
GAGCAGGAGCTGGCTACTGCTCAGAGTGTGGCTGACGCCCTGGGTTCTGGCTTCAACCCAGCAGGGGCCAGC  
GGGACCAAGCCCCACATTCACTTGTCACTGCTTGAACCTATTATTTGTATTGAAACAGAGTTATGCT  
AACTATTATAGATTGTTAATTAAAGCTGTGATTTCAAGGTTATTATTTATTGATTTATGTTCAATGGT  
GATTGTAACCTCCCAAGGCCGCCAGTGGGATGGGAGGGAGGAGGAGAAGGGGGCTGGCCGCTGCAGTCACATCT  
GTCCAGAGAAATTCTTTGGGACTGGAGGGAGGAGAAGGGGGCTGGCCGCTGCAGTCACATCT  
GTTGGGGAGGGCTGGCCCTGGCTTCAAGGGTTGACTGGGGCTGGAGAGAGAGGGAGGAAACCTCAAT  
AACCTTGAAGGTGGAATCCAGTTATTCTCTGGCTGCAGGGTTCTTATTACTCTTCTGAATGTCAAGGCAG  
TGAGGTGCCCTCACTGTGAATTGTGGTGGCGGGGCTGGAGGAGGGTGGGGGCTGGCTCCGTCCCTCCAGC  
CTTCTGTGCCCTGCTTAACAAATGCCGCCAAGTGGCACCTCACGGTTGCACTTCAATTCCACCAAGATGACCTGA  
TGAGGAAATCTCAATAGGTGCAAAGATGCAAAATTGTTATATGAAACATATAACTGGAGTCGTAAAAAG  
CAAATTAAGAAGAATTGGACGTTAGAAGTTCTATTAAAGCAGCTTCTAATAAGTTGTTCAAAGCTGAAAAAA  
AA

## **FIGURE 58**

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKDLGQLDFEEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEKILKSMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMWWRHLVAGGGAGAVSRTCTAPLDRLKVLQMVKHASRSNNMGIVGGFTQMIREGGARSLWRGNGINVLKIAPESAIKFMAYEQIKRLVGSQETLRIHERLVAGSLAGAIAQSSIYPMEVLKTRMALRKTGQYSGMILDCARRILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNSADPGVFVLLACGTMSSCQQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFGLYRGLAPNFMKVI PAVSISYVYENLKITLGVQSR

**Important features:**

**Signal peptide:**

amino acids 1-16

**Putative transmembrane domains:**

amino acids 284-304, 339-360, 376-394

**Mitochondrial energy transfer proteins signature.**

amino acids 206-215, 300-309

**N-glycosylation sites.**

amino acids 129-133, 169-173

**Elongation Factor-hand calcium-binding protein.**

amino acids 54-73, 85-104, 121-140

## FIGURE 59

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGAACCTCCCCAGCCATGGC  
TTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTG  
CACTCATCATTGGCTTGGTATTCAGGGAGACACTCCATCACAGTCACTACTGTCGCCTCAGCT  
GGGAACATTGGGGAGGATGGAATCCTGAGCTGCACTTTGAACCTGACATCAAACATTCTGATAT  
CGTGATACAATGGCTGAAGGAAGGTGTTAGGCTTGGCATGAGTCAGGAAAGGAAAGGAAAGATG  
AGCTGTCGGAGCAGGATGAAATGTTAGGCTTGGCATGAGTCAGGAAAGGAAAGGAAAGATG  
GGCAATGCCCTTTGCGGCTGAAAAACGTCAACTCACAGATGTCGGCACCTACAAATGTTATAT  
CATCACTTCTAAAGGCAAGGGAAATGCTAACCTTGAGTATAAAACTGGAGCCTTCAGCATGCCGG  
AAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTGCCTGTGAGGCTCCCCGATGGTCCCC  
CAGCCCCACAGTGGCTGGGATCCCAAGTTGACCAGGGAGCCAACCTCTCGGAAGTCTCAAATAC  
CAGCTTGAGCTGAACTCTGAGAATGTGACCATGAAGGTTGTCTGTGCTCTACAATGTTACGA  
TCAACAAACACATACTCCTGTATGATTGAAATGACATTGCCAAAGCAACAGGGATATCAAAGTG  
ACAGAACATCGGAGATCAAAAGGCGGAGTCACCTACAGCTGCTAAACTCAAAGGCTCTGTGT  
CTCTTCTTCTTGCATCAGCTGGCACTTCTGCCTCTAGCCCTTACCTGATGCTAAATAAAT  
GTGCCTTGGCCACAAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTCAC  
CACCAAGATATGACCTAGTTTATATTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTG  
AGCAAACAAGAGCAAGAAACAAAAAGAAGCCAAAGCAGAAGGCTCCAATATGAACAAGATAAT  
CTATCTCAAAGACATATTAGAAGTTGGGAAATAATTCAATGTGAACATAGACAAGTGTGTTAAGA  
GTGATAAGTAAATGCACGTGGAGACAAGTCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGT  
CACCTGGGAGTGGAGGACAGGGATAGTCATGTTCTGTCTGAATTGGTATATGTC  
TGTAATGTTGCTCTGAGGAAGCCCCCTGGAAAGTCATCCAAACATATCCACATCTTATATTCCAC  
AAATTAAGCTGTAGTATGTACCCCTAACAGCCTGCTAATTGACTGCCACTCGCAACTCAGGGCG  
GCTGCATTTAGTAATGGGTCAAATGATTCACCTTTATGATGCTCCAAAGGTGCCTTGGCTTC  
TCTTCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTAGCATAAACAGAGCAGT  
CGGGGACACCGATTTATAAATAAACTGAGCACCTTCTTTAAACAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 60**

MASLGQILFWSIISIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLS  
DIVIQWLKEGVGLVHEFKEGKDELSSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTDAGTYKC  
YIITSKGKGNANLEYKTGAFSMPEVNVDYNASSETLRCEAPRWFPQPTVVWASQVDQGANFSEVS  
NTSFELNSENVTMKVVSVLYNVTINNTYSCMIENDIAKATGDIKTESEIKRRSHLQLLNASKASL  
CVSSFFAISWALLPLSPYIMLK

**Important features:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 258-281

**N-glycosylation sites.**

amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220,  
220-224

**N-myristoylation sites.**

amino acids 52-58, 126-132, 188-194

## **FIGURE 61**

TGACGTCAGAATCACCATGGCAGCTATCCTTACCGGCAGGGCTGCCAGGAGCTGCAGGACAAG  
CACCAAGGAGCCCTCCGGTAGCTACTACCCCTGGACCCCCAATAGTGGAGGGCAGTATGGTAGT  
GGGCTACCCCTGGTGGTTATGGGGCTGCCCCCTGGAGGGCTTATGGACCACAGCTGG  
TGGAGGGCCATGGACACCCAATCCTGGATGTTCCCCTGGAACCTCAGGAGGACCATATG  
GCGGTGCAGCTCCGGGGCCCTATGGTCAGCCACCTCCAAGTCCCTACGGTGCCAGCAGCCT  
GGGTTTATGGACAGGGTGGCCCTCCAATGTGGATCCTGAGGCCTACTCTGGTCCAGTC  
GGTGGACTCAGATCACAGTGGCTATATCTCATGAAGGAGCTAAAGCAGGCCCTGGTCAACTGCA  
ATTGGTCTTCATTCAATGATGAGACCTGCCATGATGATAAACATGTTGACAAGACCAAGTCA  
GGCCGCATCGATGTCACGGCTCTCAGCCCTGTGGAAATTCACTCCAGCAGTGGAAAGAACCTCTT  
CCAGCAGTATGACCGGGACCGCTGGCTCCATTAGCTACACAGAGCTGCAGCAACCTCTGTCCC  
AAATGGGCTACAAACCTGAGCCCCAGTTCACCCAGCTCTGGTCTCCGCTACTGCCACGCTCT  
GCCAATCCTGCCATGCAGCTTGACCGCTTCATCCAGGTGTGCACCCAGCTGCAGGTGCTGACAGA  
GGCCTCCGGGAGAAGGACACAGCTGTACAAGGCAACATCCGCTCAGCTTGAGGACTTCGTCA  
CCATGACAGCTCTCGGATGCTATGACCAACCATCTGTGGAGAGTGGAGTGCACCAAGGGACCTT  
TCCTGGCTTCTTAGAGTGAGAGAAGTATGTGGACATCTTCTTCTGTCCCTCTAGAAC  
ATTCTCCCTGCTGATGCAACACTGTTCCAAAAGAGGGTGGAGAGTCCCTGCATCATAGCCACCA  
AATAGTGAGGACCGGGCTGAGGCCACACAGATAGGGCCTGATGGAGGAGAGGATAGAAC  
ATGTCCTGATGGCCATGAGCAGTTGAGTGACCCAGCTGGCACCAGGAGCAGGTCTTGTAA  
AGTTAGTGTCCAGTCAGCTGAGCTCCACCCCTGATGCCAGTGGTAGTGTTCATGGCTGTTACC  
GTTAGTACCTGTGTTCCCTCACCAGGCCATCCTGTCACAGCAGCCATTCTCCAAAGTGGAA  
CTGACCAAGCATGAGAGAGATCTGTCTATGGGACCAAGTGGCTGGATTCTGCCACACCCATAA  
CCTTGTGTGTTAACTCTAGCTGCCCTGGGCTGGCCCTGCTCAGACAAATCTGCTCCCTGGC  
CTTGCCAGGCTCTGCCCTGCAGCTGGGACCCCTCACTTGCCCTGCCATGCTCTGCTCGG  
TCAGTCTCCAGGAGACAGTGGTCACCTCTCCCTGCCAATACTTTTTAATTGCA  
ATTGGGGC  
AAAGTCCAGTGAAATTGTAAGCTCAATAAAAGGATGAAACTCTGA

## **FIGURE 62**

MASYPYRQGCPGAAGQAPGAPPGSYYPGPPNSGGQYGSGLPPGGYGGPAPGGPYGPPAGGGPYG  
HPNPGMFPSTGPGPYGGAAPGGPYGQPPPSSYGAQQPGLYGQGGAPPNVDPEAYSWFQSVDSDH  
SGYISMKELKQALVNCNSSFNDETCLMMINMFDKTKSGRIDVYGFSAWKFIQQWKNLFQQYDR  
DRSGSISYTELQQALSQMGYNLSQFTQLLVSRYCPRSANPAMQLDRFIQVCTQLQLTEAFREK  
DTAVQGNIRLSFEDFVTMTASRML

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation site.**

amino acids 147-150

**Casein kinase II phosphorylation sites.**

amino acids 135-138, 150-153, 202-205, 271-274

**N-myristoylation sites.**

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-66, 70-75, 78-83, 83-88, 87-92, 110-115

### **FIGURE 63**

## **FIGURE 64**

MQGRVAGSCAPLGLLVCLHLPGLFARSIGVWEEKVSQNFQGTNL PQLGQPSSTGPSNSEHPQPAL  
DPRSNDLARVPLKLSVPPSDGFPPAGGSAVQRWPPSWGLPAMDSWPEDPWQMMAAAEDRLGEA  
LPEEELSYLSSAAALAPGSGPLPGESSPDATGLSPEASLLHQDSESRLPRSNSILGAGGKILSQRP  
PWSLIHRVLPDHPWGTLNPSVSWGCCCCGTGWRPMMPHPEGIWGINNQPPGTWGNINRYPGGS  
WGNINRYPGGSWGNINRYPGGSWGNIHLYPGINNPFPGVLRPPGSSWNIPAGFPNPPSPRLQWG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Casein kinase II phosphorylation sites.**

amino acids 56-59, 155-158

**N-myristoylation sites.**

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263,  
259-264, 269-274, 270-275, 280-285, 281-286, 305-310

## **FIGURE 65**

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGTC  
TGGGCTGCCCTTGTCCCTCCTTGCACCTGGCAGCTCACATGGAACAGGGCCGGGTATGA  
CTTGCAACTGAAGCTGAAGGAGTCTTCTGACAAATTCCCTCATGAGTCCAGCTCCTGGAA  
TTGCTTGAAAAGCTCTGCCTCCCTCCATCTCCCTCAGGGACCAGCGTCACCCCTCCACCATGC  
AAGATCTCAACACCATGTTGTCGAACACATGACAGCCATTGAAGCCTGTGTCCTTGGCC  
GGGCTTTGGGCCGGGATGCAGGAGGCAGGCCCGACCCCTGTCTTCAGCAGGCCACCC  
CTGAGTGGCAATAAATAAAATTGGTATGCTG

## **FIGURE 66**

MGSGPLVLLTLLGSSHGTGPGMTLQLKLKESFLTNSSYESSFLELLEKLCLLLHLPSGTSVTL  
HHARSQHHVVCNT

**Important features:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation site.**

amino acids 37-41

**N-myristoylation sites.**

amino acids 15-21, 19-25, 60-66

## **FIGURE 67**

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCGGC  
CAGGTGCCCGTCCAGGTGCCCTGGCCGGAGATGCGGTAGGAGGGCGAGCGCGAGAACCCCC  
TTCCTCGCGCTGCCAACCCGCCACCCAGCCATGGCGAACCCCGGGCTGGGCTGCTCTGGCG  
CTGGGCTGCCGTTCTGCTGGCCGCTGGGGCGAGCCTGGGGCAAATACAGACCACCTCTGC  
AAATGAGAATAGCACTGTTGCCTTCATCCACCAAGCTCCAGCTCCAGCTGGCAACCTGCGTCCGG  
AAGCCATCACTGCTATCATCGTGGTCTTCCCTCTGGCTGCCTTGCTCCCTGGCTGTGGGCTG  
GCACTGTTGGTGGGAAGCTTCGGAGAACGGCAGACGGAGGGACCTACCGGCCAGTAGCGA  
GGAGCAGTTCTCCATGCAGCCAGGCCCCCTCAGGACTCCAAGGAGACGGTGCAGGGCT  
GCCTGCCCATCTAGGTCCCTCTGCATCTGTCTCCCTCATTGCTGTGACCTTGGGAAA  
GGCAGTGCCCTCTGGCAGTCAGATCCACCCAGTGCTTAATAGCAGGGAAAGAAGGTACTCAA  
AGACTCTGCCCTGAGGTCAAGAGAGGATGGGCTATTCACTTTATATTTATATAAAATTAG  
TAGTGAGATGTAaaaaaaaaaaaaaaa

## **FIGURE 68**

MANPGLGLLLALGLPFLARWGRAWGQIQTTSANENSTVLPSSSSDGNLRPEAITAIIVFS  
LLAALLLAVGLALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

**Important features:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 56-80

**N-glycosylation site.**

amino acids 36-40

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 86-90

**Tyrosine kinase phosphorylation site.**

amino acids 86-94

**N-myristoylation sites.**

amino acids 7-13, 26-32

**FIGURE 69**

## FIGURE 70

MGLFRGFVFLVLCLLHQSNNTSFIKLNNGFEDIVIVIDPSVPEDEKIIEQIEDMVTTASTYLFE  
ATEKRFKKNVSIILIPENWKENPQYKRPKHENKHADVIVAPPTLPGRDEPYTKQFTECGEKG  
EYIHFTPDLGGKKQNEYGPPGKLFWHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATRC  
SAGISGRNRYVYKCQGGSCLSRACRIDSTTKLYGKDCQFPDKVQTEKASIMFMQS  
IDS VVEFCNEKTHNQEAPSLQNIKCNFRSTWEVISNSED  
FKNTIPMVTPPPPVFSLLKISQRIVCLVLDKSGSMGGKDRLNR  
MNQAAKHFLQLQTENGWSWGMVHFSTATIVNKLIQIKSSDERNTLMAGLPTYPLGGTS  
SICSGIKYAFQVIGELHSQLDGSEVLLTDGEDNTASSCIDEVKQSGAIVH  
FIALGRAADEAVIEMS  
KITGGSHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLTLNSNAWMNDT  
VIIDSTVGKDTFFLITWNSLPPSISLWDPSGTIMENFTV  
DATSKMAYLSIPGTA  
KVG  
TWAYNLQAKANPETLTITV  
TSRAANSSVPPITVNAKMNDVNSFPSPMIVYAEILQGYVPVLGANV  
TAFIESQNGHTEV  
LELLDNGAGADSF  
KNDGVYSRYFTAYTENG  
RYSLKVR  
AHGGANTARLKL  
RPLNRAAYIPG  
WV  
VNGEIEANPPRPE  
IDE  
DTQTT  
LED  
FSRTASGGAF  
VV  
SQVPSLPL  
DQYPP  
SQITD  
L  
DATV  
HEDK  
I  
LT  
WT  
APGDN  
FDVGKV  
QRYIIR  
ISAS  
ILD  
RDS  
FDD  
ALQV  
NT  
D  
LSP  
KEANS  
KES  
FAF  
K  
PEN  
I  
SEEN  
A  
THI  
FIA  
KS  
ID  
K  
SNL  
TSK  
V  
SNIA  
QV  
TL  
F  
IP  
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I

**Signal peptide:**

amino acids 1-21

**Putative transmembrane domains:**

amino acids 284-300, 617-633

**Leucine zipper pattern.**

amino acids 469-491, 476-498

**N-glycosylation site.**

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592, 628-632, 811-815, 832-836, 837-841, 852-856, 896-900

## FIGURE 71

CTCCCTTAGGTGGAAACCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAAGACCATACGTCCCCGGGCAGGGGTGA  
CAACAGGTGTCATCTTTGATCTCTGTGTGCTGCCCTCCTAATTCAAGGAAAGACGCCAAGGTAAATTGACCCA  
GAGGAGCAATGATCTAGGCCACCTCCCTAACCCTCCCTTGAAACCCCAAGTATGCCAGGATTACTAGAGAGTGTCA  
ACTCAACCAGCAAGCGGCCTTCGGCTTAACCTGTGGTGGAGGAGAAACCTTGTGGGGCTCGGTTCTTAGCA  
GTGCTCAGAAGTGAATTGCTGAGGGTGGACAGAAGAAAGGAAAGGTCCCTCTGCTGTGGCTGCACATCAGGAA  
GGCTGTGATGGGAATGAGGTGAAACTTGGAGATTCACTCGTATTGCTCTGCTGCAGATCATCCTTAA  
AGTAGAGAAGCTGCTCTGTGTTGTTAAGTCAAGGAGGAGAACTCGTTAGAAGGAAATGGATGCAAGCAGCTC  
CGGGGGCCCAAACCGCATGCTTCTGTGGCTAGCCAGGGAAAGCCCTCCGTGGGGCCCGGCTTGAGGGATGCC  
ACCGGTTCTGGACGCATGGCTGATTCTGAATGATGATGGTCGCCCCGGGCTGCTTGCGTGGATTTCGGGGTGGT  
GTTTGCTGGTGCCTCTGCTGTGCTATCTGCTGTACATGTGGGCTGCACCCCAAAAGGTGACGAGGAGCAG  
CTGGCACTCAGGCAAGGGCAACAGCCACGGGAAGGGGAGGGTACCCAGGGCTCCTCAGGAGTGGGAGGAGCAG  
CCCAACTAGTGAGGAGCTGAAGGGAGATGCCACAGCTCAAGGAGGAGTGCAGGAGAGGAGTGAGCAGCTCAG  
AATGGGCAGTACCAAGCAGGGATGCTGCTGGCTGGGCTGGACAGGAGCCCCAGAGAAAACCCAGGCCACCTC  
CTGGCCTCTGCACTCGCAGGGACAAGGCAGGGTGAATGCTGGCGTCAAGCTGGCACAGAGTATGAGCAGTG  
CCTTCGATAGCTTACTCTACAGAAGGTGACCGAGCTGGGAGACTGGCTTACCCGCCACCCGGAGGAGAACCTGTG  
AGGAAGGAAAGCAGGGATGAGTTGGGAGGATTGAATCAGCCTGGAGACCTGAAACAATCTGCAGAGAACAGC  
CCCAATCACGGCTTACAGGCTCTGATTTCATAGGAGATCTCCAGAACAGAAAGGGACAAAGGACATTGTAT  
GAGCTCACCTCAAAAGGGACCAAACAGCAATTCAACGGCTCATCTTATTGACCATTCAGCCCCATCATGAAA  
GTAAAAAAATGAAAGCTCAACATGGCAACACGCTTATCAATGTTATGTCGCTCTAGCAAAAGGGTGGACAAGTTC  
CGGCAGTCTATGAGAAATTCTAGGGAGATGTCAGTGGAGGATGGAGACTCCATCTACTGTTGTTTACTTGGG  
AAAGAAGAAATAATGAAAGTCAAGGAATACTGAAACACTTCAAGGCTGCCAACCTCAGGAACCTTACCTTCATC  
CAGCTGAATGGAGAAATTCTCGGGGAAACTGGGACTGATGTTGGAGGGCTCTGGAGGAAACGTCCTTC  
TTTTCTGTGATGGACATCTTCACTTCACATCTGATTCTCAATACCTGTAGGCTGAATACACAGGGAGAAG  
GTATTTATCAGTTCTTCTGCTAGTCACTGACAATCTGGCATAATATACGGCACCATGATGCACTCCCTCCCTGGAA  
CAGCAGCTGGTCTAAAGAAGGAAACTGGGATTTGGAGAGACTTGGGATGACGTGTCAGTATCGGTCAAGAC  
TTCATCAATAGTGGGTTGATCTGGACATCAAAGGCTGGGGAGGAGATGTCACCTTATCGCAAGTATCTC  
CACACCCACTCATAGTGGTACGGACCCCTGCGCAGGACTCTTCACCTCTGGCATGAGAACGGCTCATGGAG  
CACAGCAACCTCATAGTGGTACGGACCCCTGCGCAGGACTCTTCACCTCTGGCATGAGAACGGCTCATGGAG  
CTGACCCCCGACAGTACAGATGTCAGTCAGTCAGGCAAGGCGATGCCACGGCAGCTGGCATGCTG  
GTGTTCAAGGACAGATAGGGCTCACCTCGCAAAACAGAAAGACAAGTAGCAAAACATGAACCTCCAGA  
GAAGGATGTGGGAGACACTTTTCTTCTGGCAATTACTGAAAGTGGCTGAAACAGAGAAAAGACTTCCATAAA  
GGAGCAGAAAAGGAAATTGGACTGATGGTCAAGAGATGAGAAAGCCTGGGATTTCTCTGTTGGGCTTTTACAACAGA  
AATCAAATCTCGCTTGCCTGCAAAAGTAACCCAGTGCACCTCTGAAGTGTCTGACAAAGGAGAAATGCTGTG  
AGATTATAAGCTTAATGGTGGAGGTTGATGGTTAACATACACTGAGACCTGTTGTTGTGCTCATTGA  
AATATTICATGATTTAAAGAGCAGTTTGTAAAAAATTCAATTAGCATGAAAGCAAGCATATTCTCCTCATATGAATGA  
GCCTATCAGCAGGGCTAGTTCTAGGAATCTAAATATCAGAAGGAGCAGGAGAGGAGATAGCCTTATTATGACT  
AGTGAATACATTAAGTAAATAAAATGGACAGAAAAGGAAACCATAAATATCGTGTATTTCCCAAGAT  
TAACCAAAATACTCGTTATCTTGGTCTCTTAAACTCTCCCTTTTCTTTTATTTAAATGCACT  
TTTTCTCGTTGAGTTATAGTCTGTTATTAACTTACACTTGCAGCCTAACAGGACAAGTGGCCTAC  
ATTTTTATATTAAAGAAGATACTTGAGATGCAATTGAGAACTTCAAGCTAAAGCATCAATTGATGCCATAT  
CCAAGGACATGCCAAATGCTGATTCTGCAAGGACTGAATGTCAGGCATTGAGACATAGGGAAAGGAATGTTGACT  
AATACAGACGTACAGATACTTCTGTAAGGATATTTCGAAGAGGAGCAACTGAAACACTGGAGGAAAAGAAAATGAC  
ACTTCTCGTTGAGGACCCCTTACCTGTTAAATAACCAAGTATACCGTGTGATATGTCAGTACCTAAAGTCAGAAACCACTT  
CTCCTCAGAGTAGGGACCCCTTACCTGTTAAATAACCAAGTATACCGTGTGACCCAAACATCTCTTTC  
AAAACAGGGTGTCTCTCTGGCTTCTGGCTTCCATAAGAAGGAAATGGAGAAAATATATATATATATATATTGT  
GAAAGATCAATCCATCTGCCAGAATCTAGTGGGATGGAAGTTTCTACATGTTATCCACCCAGGCCAGGGAG  
TAACTGAATTATTAAATAAGCAGTTCTACTCAATCACCAGATGCTTCTGAAAGTGTGTTTATTACCAATT  
CAAACATTAAGGAAACATTAACAGTAAACATAGTGGTTCTTCATTGATGTTGAAAGTATTAGCCAGCACAG  
ATGCATGAGCTAATATCTCTTGTGTTAAATAAGCATTGTATTGATTGATTGACTGGTAGTTATGAAATTAAACACAGG  
ATTCAAGCTGTTGGTGTGTTAAATAAGCATTGTATTGATTGACTGGTAGTTATGAAATTAAACACAGG  
CCATGAATGGAAGGTTGATTGACAGCTAATAAAATGATTGTTGATGAA

## **FIGURE 72**

MMMVRRGLLAWISRVVLLVLLCC AISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQEWE  
EQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFLHSQVDK  
AEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVRKDRDELVEAIESALETLNNP  
ENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPIMKVNEKLNMAN  
TLINVIVPLAKRVDKFRQFMQNFR EM CIEQDGRVHLTVYFGKEEINEVKGILENTSKAANFRNF  
TFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKVFYPVLFQY  
NPGIIYGHDAVPPLEQQQLVIKETGFWRDFGFGMT CQYRSDFINIGGF DLDIKGWGGEDVHLYR  
KYLHSNLIIVRTPVRGLFHLWHEKRCMDELTP EQYKMCMQSKAMNEASHGQLGMLVFRHEIEAHL  
RKQKQKTSSKKT

**Important features:**

**Signal peptide:**

amino acids 1-27

**N-glycosylation sites.**

amino acids 315-319, 324-328

**N-myristylation sites.**

amino acids 96-102, 136-142, 212-218, 311-317, 339-345, 393-399

**Amidation site.**

amino acids 377-381

## **FIGURE 73**

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGGCAGCAAGAGAGTTGTCTGGGATCCA  
GAAACCCATGATAACCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGAGACAGCAAGA  
GAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCACTCCTC  
CCTCCCTCTCTGCCTGCTCTAGTCCTAGTCCTCAAATTCCAGTCCCCTGCACCCCTTC  
CTGGGACACTATGTTGTTCTCCGCCCTCTGCTGGAGGTGATTGGATCTGGCTGCAGATGGGG  
GTCAACACTGGACGTATGAGGGCCACATGGTCAGGACCATGGCCAGCCTCTTACCCGTAGTGT  
GGAAACAATGCCAGTCGCCATCGATATTCAACAGACAGACTGTGACATTGACCCGTGATTTGCC  
TGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGCCTTGGACCTGCACAACAATGCC  
ACACAGTCAACTCTCTGCCCTCTACCCGTATCTGGGTGGACTTCCCCGAAAATATGTAGCT  
GCCAGCTCCACCTGCACTGGGTAGAAAGGATCCCCAGGGGGTCAGAACACCAAGATCAACAG  
TGAAGCCACATTGCAAGAGCTCCACATTGTACATTATGACTCTGATTCTATGACAGCTTGAGTG  
AGGCTGCTGAGAGGCCTCAGGGCTGGCTGGCATCTAATTGAGGTGGTGAGACTAAG  
AATATAGTTATGAACACATTGAGTCACCTGCATGAAGTCAGGCATAAAGATCAGAACACTC  
AGTGCCTCCCTCAACCTAACAGAGAGCTGCTCCCCAACAGCTGGGCAGTACTCCGCTACAATG  
GCTCGCTCACAACTCCCCCTGCTACCAAGAGACTGCTGGACAGTTTTATAGAAGGTCCAG  
ATTTCAATGGAACAGCTGGAAAGCTTCAGGGGACATTGTTCTCCACAGAACAGGGAGCCCTCTAA  
GCTTCTGGTACAGAAACTACCGAGCCCTCAGCCTCTCAATCAGCGCATGGCTTGCTTCTTCA  
TCCAAGCAGGATCCTCGTATACCAACAGGTGAAATGCTGAGTCTAGGTGAGGAATCTGGTTGGC  
TGTCTGCCTTCCTGGCTGTTATTCATTGCTAGAAAGATTGGAAGAACAGGGCTGGAAAA  
CCGAAAGAGTGTGGATGACTCCCTTCATGCCATCAGAACAGCCACGACTGAGGCATAAATTCTCTCAGATAC  
CATGGATGTGGATGACTCCCTTCATGCCATCAGAACAGCCACGACTGAGGCATAAATTCTCTCAGATAC  
CCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCTCCCTGGACATCTTAGAGAGGAAT  
GGACCCAGGCTGTCAATTCCAGGAAGAACTGCGAGGCCTCAGCCTCTCCAAACATGTAGGAGGAA  
ATGAGGAAATCGCTGTGTTAATGCAGAGANAAACTCTGTTAGTGCAGGGGAAGTTGGG  
ATATAACCCCAAAGTCCCTACCCCTCACTTTATGGCCCTTCCCTAGATATACTGCGGGATCT  
CTCCTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTGATCAATATATTTGGAAATTAAAG  
TTTCTGACTTT

## **FIGURE 74**

MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFPDPALQ  
PHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEAT  
FAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPP  
FNLRELLPKQLGQYFRYNGSLTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEEPSKLLV  
QNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYFIARKIRKKRLENRKS  
VVFTSAQATTEA

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 291-310

**N-glycosylation site.**

amino acids 213-216

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 197-245, 104-140, 22-69

## **FIGURE 75**

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCCCTGGGACGGGCAGTCCCTGTGTC  
TCTGGTGGTTGCCTAAACCTGCAAACATCACCTTATCCATCAACATGAAGAATGCCTACA  
ATGGACTCCACCAGAGGTCTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTCA  
ATTGGGCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTCTGTTGCTGACAGCTCC  
AGAGAAGTGGAAAGAGAAATCCAGAAGACCTCCTGTTCCATGCAACAAATATACTCCAATCTGA  
AGTATAACGTGTCTGTTGAATACTAAATCAAACAGAACGTGGTCCAGTGTGACCAACCAC  
ACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTACTGCGTACACGTGGAGTCCTCGTCCC  
AGGGCCCCCTCGCCGTGCTAGCCTCTGAGAACAGCAGTGTGCCAGGACTTGAAAGATCAATCAT  
CAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTGCCATATCTATTACCGTGTCTTT  
TCTGTGATGGGCTATTCCATCTACCGATATCCACGTGGCAAAGAGAAACACCCAGCAAATT  
GATTTGATTATGGAAATGAATTGACAAAAGATTCTTGTGCCTGCTGAAAAAAATCGTGATTA  
ACTTTATCACCTCAATATCTGGATGATTCTAAAATTCTCATCAGGATATGAGTTACTGGGA  
AAAAGCAGTGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGA  
GGAAGAGGAGGTGAAACATTAGGTATGCTCGCATTGATGGAATTGGTGA  
AAAACACGGAAGGTACTCTCTCACCCAGCAAGAGTCCTCAGCAGAACAAACCCCCGGATAAA  
ACAGTCATTGAATATGAATATGATGTCAGAACCACTGACATTGTCGGGGCCTGAAGAGCAGGA  
GCTCAGTTGCAGGAGGGTGTCCACACAAGGAACATTGGAGTCGCAGGCAGCGTTGGCAG  
TCCTGGGCCGAAACGTTACAGTACTCATACACCCCTCAGCTCAAGACTTAGACCCCTGGCG  
CAGGAGCACACAGACTCGGAGGAGGGCCGGAGGAAGAGCCATCGACGACCCGGTCACTGGGA  
TCCCCAAACTGGCAGGCTGTGTATTCCCTCGCTGTCCAGCTCGACCAGGATTAGGGCTGGCG  
AGCCTCTGAGGGGGATGGCCTGGAGAGGGAGGGTCTCTATCTAGACTCTATGAGGAGCCGGCT  
CCAGACAGGCCACAGGAGAAAATGAAACCTATCTCATGCAATTGCAAGGAAATGGGGTTATA  
TGTGCAGATGGAAAACTGATGCCAACACTCCCTTGCCTTGTGCAAACAAAGTGAG  
TCACCCCTTGATCCCAGCCATAAGTACCTGGGATGAAAGAAGTTTCCAGTTGTCA  
CTGTGAGAATTACTTATTCTCTATTCTCATAGCACGTGTGATTGGTCATGCATGTA  
GGTCTCTTAACAATGATGGTGGCCTCTGGAGTCAGGGCTGGCCGGTGTCTATGCAGAGAA  
AGCAGTCAATAATGTTGCCAGACTGGGTGCAGAATTATTAGGTGGGTGT

## **FIGURE 76**

MSYNGLHQRVFKELKLLTLCISISSQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIY  
SNLKYNVSVLNTKSNRTWSQCVTNHTLVLWLEPNTLYCVHVESFVPGPPRRAQPSEKQCARTLK  
DQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYGNEDDKRFFVPAEK  
IVINFITLNISDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEVKHTMLGYASHLMEIFC  
DSEENTEGTSLTQQESLSRTIPPDKTVIEYEYDVRTTDICAGPEEQELSLOQEEVSTQGTLLSQA  
ALAVLGPQTLQYSYTPQLQDLDPLAQEHTDSEEGPEEEPSTTLVDWDPQTGRLCIPSLSFDQDS  
EGCEPSEGDSLGEEGLLSRLYEEPAPDRPPGENETYLMQFMEEWGLYVQMAN

**Important features:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 140-163

**N-glycosylation sites.**

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

## **FIGURE 77**

GAGGAGCGGGCCGAGGACTCCAGCGTGCCCAGGTCTGGCATCCTGCAC TTGCTGCCCTTGACAC  
CTGGGAAGATGGCCGGCCCGTGGACCTTCACCCCTCTGTGGTTGCTGGCAGCCACCTTGATC  
CAAGCCACCCCTCAGTCCCAC TGCA GTTCTCATCCTCGGCCAAAAGTCATCAAAGAAAAGCTGAC  
ACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGTGCTCAGTGCCATGC  
GGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGCAGCTGGTGAACACCGTCTGAAGCACATC  
ATCTGGCTGAAGGTCACTCACAGCTAACATCCTCCAGTCAGGTGAAGGCCCTGCCAATGACCA  
GGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCTGGTCAAGACCA  
TCGTGGAGTTCCACATGACGACTGAGGCCAAGGCCACCATCCGCATGGACACCAGTGCAAGTGGC  
CCCACCCGCCTGGCCTCAGTGACTGTGCCACCGCCATGGGAGCCTGCGCATCCAAC TGCTGTA  
TAAGCTCTCCTTCTGGTGAACGCCCTAGCTAACAGGTCAACCTCTAGTGCATCCCTGC  
CCAATCTAGTGA AAAACCCAGCTGTGTCCCGTATCGAGGCTCCTCAATGGCATGTATGCAGAC  
CTCCTGCAGCTGGTGAAGGTGCCATTCCCTCAGCATTGACCGTCTGGAGTTGACCTTGTGA  
TCCTGCCATCAAGGGTGAACCAATT CAGCTCACCTGGGGCCAAGTTGGACTCACAGGAA  
AGGTGACCAAGTGGTTCAATAACTCTGCAGCTTCCCTGACAATGCCACCCCTGGACAACATCCG  
TTCAGCCTCATCGTGAGTCAGGACGTGGTGAAGCTGCAGTGGCTGCTGTCTCCAGAAGA  
ATTCAATGGCCTGGTGGACTCTGTGCTCCTGAGAGTCGCCATCGGCTGAAGTCAAGCATTGGC  
TGATCAATGAAAAGGCTGCAGATAAGCTGGATCTACCCAGATCGTAAGATCTAACCTCAGGAC  
ACTCCCGAGTTTTTATAGACCAAGGCCATGCCAAGGTGGCCAACTGATCGTGTGGAAAGTGT  
TCCCTCCAGTGAAGGCCCTCCGCCCTTGTCAACCTGGCATCGAACGCCAGCTCGGAAGCTCAGT  
TTTACACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTGTGATCGGATCCAGCTG  
ATGAACCTGGGATTGGCTGGTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCCA  
CTCCATCCTGCTGCCGAACCAGAAATGCCAATTAAAGATCTGGGGTCCCAGTGTCAATTGGTGAAGG  
CCTTGGGATTCGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTGTGCTTACTCCAGCCTCC  
TTGTGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTGGATGGCAGCCATCAGGGAAAGGCTGG  
GTCCCAGCTGGGAGTATGGGTGTGAGCTATAGACCAATCCCTCTGCAATCAATAAACACTTG  
CCTGTGAAAAA

## **FIGURE 78**

MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPVKIKEKLTQELKDHNATSILQQLPLLSAMREK  
PAGGIPVLGSLVNTVLKHIWLKVITANIILQLQVKPSANDQELLVKIPLDMVAGFNTPLVKTIVE  
FHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMNLLVPSLPNL  
VKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYLGAKLDSQGKVT  
KWFNNNSAASLTMPTLDNIPFSLIVSQDVVKAAVAAVLSPEEFMVLLDSVLPESAHRLKSSIGLIN  
EKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSEALRPLFTLGIASSEAQFYT  
KGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIHSILLPNQNGKLRSGVPVSLVKALG  
FEAAESSLTKDALVLTPASLWKPSSPVSQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 48-51, 264-267, 401-404

**Glycosaminoglycan attachment site.**

amino acids 412-415

**LBP / BPI / CETP family proteins.**

amino acids 407-457

## **FIGURE 79**

GAGAGAAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGAGC  
TTCAGCCTGAAGACAAGGGAGCAGTCCTGAAGACGCTCTACTGAGAGGTCTGCCATGGCCTCT  
CTTGGCCTCCAACCTGTGGGCTACATCCTAGGCCTCTGGGCTTTGGGACACTGGTGCCAT  
GCTGCTCCCCAGCTGGAAAACAAGTTCTTATGCGGTGCCAGCATTGTGACAGCAGTTGGCTCT  
CCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATACCCAGTGTGACATCTATAGC  
ACCCTCTGGGCCTGCCGCTGACATCCAGGCTGCCAGGCCATGATGGTGACATCCAGTGCAAT  
CTCCTCCCTGGCCTGCATTATCTCTGTTGGCATGAGATGCACAGTCTTCTGCCAGGAATCCC  
GAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTCATCCTGGAGGCCCTGGGATTC  
ATTCCGTGTCCTGGAATCTCATGGGATCCTACGGGACTCTACTCACCACGTGGCCTGACAG  
CATGAAATTGAGATTGGAGAGGGCTTTACTTGGGATTATTCTCCCTGTTCTCCCTGATAG  
CTGGAATCATCCTCTGCTTTCCCTGCTCATCCAGAGAAATCGCTCCAACACTACGATGCCCTAC  
CAAGCCCAACCTCTGCCACAAGGAGCTCTCAAGGCCGGTCAACCTCCAAAGTCAGAGTGA  
GTTCAATTCCCTACAGCCTGACAGGTATGTGTGAAGAACCAAGGGGCCAGAGCTGGGGGTGGCTG  
GGCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGT  
GTCAGAAGGTGCTGCTGAGGATAGACTGACTTGGCATTGGATTGAGCAAAGGCAGAAATGGG  
GCTAGTGTAAACAGCATGCAGGTGAATTGCCAAGGATGCTGCCATGCCAGCCTTCTGTTCC  
TCACCTTGCTGCTCCCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCATTCCCTAAGCCA  
GGACTCAGAGGATCCCTTGCCCTCTGGTTACCTGGACTCCATCCCCAAACCCACTAATCACA  
TCCCACGTGACTGACCCCTGTGATCAAAGACCCCTCTCTGGCTGAGGTTGGCTTAGCTCATT  
GCTGGGGATGGGAAGGAGAAGCAGTGGCTTGTGGCATTGCTTAACCTACTTCTCAAGCTTC  
CCTCCAAAGAAACTGATTGGCCCTGGAACCTCCATCCACTCTTGTATGACTCCACAGTGCCA  
GACTAATTGTCATGAACTGAAATAAACCATCCTACGGTATCCAGGGAACAGAAAGCAGGATG  
CAGGATGGGAGGACAGGAAGGAGCAGCCTGGACATTAAAAATA

## **FIGURE 80**

MASLGLQLVGYILGLLGLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQCD  
IYSTLLGLPADIQAAQAMMVTSSAISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVFFILGGL  
LGFIPVAWNLHGILRDFYSPLVPSMKFEIGEALYLGISSLFSLIAGIILCFSCSSQRNRSNYY  
DAYQAQPLATRSSPRPGQPPKVKEFNSYSLTGYV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 82-102, 117-140, 163-182

**N-glycosylation site.**

amino acids 190-193

**PMP-22 / EMP / MP20 family proteins.**

amino acids 46-59

## **FIGURE 81**

CCACACCGTCCGCCTCTCCCTCTGCTGGACCTTCCCTCGTCTCCATCTCTCCCTCCTTC  
CCCGCGTTCTTTCCACCTTCTTCTTCCACCTTAGACCTCCCTGCCCTCCTTCC  
GCCCACCGCTGCTTCTGGCCCTCTCGACCCCGCTCTAGCAGCAGACCTCCCTGGGTCTGTGG  
GTTGATCTGTGGCCCTGTGCCCTCCGTGTCCCTTCGCTCCCTCCGACTCCGCTCCGG  
ACCAGCGGCCTGACCCCTGGGAAAGGGATGGTCCGAGGGTGGCTCCCTCCCTTGCTGGGA  
CTCGCGCTGCTCTGGTTCCCCCTGGACTCCACGCTCGAGCCCGCCAGACATGTTGCTGCCTTT  
CCATGGGAAGAGATACTCCCCCGCGAGAGCTGGCACCCCTACTTGGAGGCCACAAGGCCTGATGT  
ACTGCCCTGCGCTGTACCTGCTCAGAGGGGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCT  
GTCCACTGCCCTGCGCTGTGACGGAGCCACAGCAATGCTGTCCTGGAAACCTCACAC  
TCCCTCTGGACTCCGGGCCCCACCAAAGTCTGCCAGCACACGGGACCATGTACCAAACGGAG  
AGATCTCAGTGCCATGAGCTTCCCTCCGCTGCCAACCCAGTGTGTGGAAACCTCACAC  
ACAGAGGGCCAGATCTACTGCCCTCACAAACCTGCCCGAACCCAGGCTGCCAGCACCCCTCCC  
ACTGCCAGACTCCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACA  
GTGTGCAGTCGCTCCATGGGGTGGACATCCTCAGGATCCATGTTCCAGTGTGCTGGAGAAAG  
AGAGGCCGGCACCCAGCCCCACTGCCCTCAGGCCCTCTGAGCTTCATCCCTGCCACTT  
CAGACCCAAGGGAGCAGGCCAGCACACTGTCAAGATCGCCTGAAGGGAGAAACATAAGAAAGCCT  
GTGTGCATGGCGGGAAAGACGTACTCCCACGGGGAGGTGTGGCACCCGGCTTCCGTGCCTTCGGC  
CCCTGCCCTGCATCCTATGCACTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCC  
CACCGAGTACCCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTGCCAGAGG  
ACAAAGCAGACCCCTGCCACAGTGAGATCAGTCTACCAGGTGTCCAAGGCACCGGGCCGGTC  
CTCGTCCACACATCGGTATCCCAAGCCCAGACAACCTGCGTCGCTTGGCCCTGGAACACGAGGC  
CTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAGATGAGGAAACTGAGGCTCAGAGAG  
GTGAAGTACCTGGCCAAGGCCACACAGCCAGAATCTCCACTTGACTCAGATCAAGAAAGTCAG  
GAAGCAAGACTTCCAGAAAGAGGGCACAGCACTTCCGACTGCTCGCTGGCCCCACGAAGGTCACT  
GGAACGTCTCCTAGCCAGACCCCTGGAGCTGAAGGTACGCCAGTCCAGACAAAGTGACCAAG  
ACATAACAAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTATTATATTAATAAAA  
TAAGAAGTTGCATTACCCCTCAAAAAAAAAAAAAAAA

## **FIGURE 82**

MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCTCSE  
GAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIFSAHELP  
PSRLPNQCVLCSCTEGQIYCGLTCPEPGCPAPLPLPDSCCQACKDEASEQSDEEDSVQSLHGVR  
HPQDPCSSDAGRKRGPGTPAPTGLSAPLSFI PRHFRPKAGSTTVKIVLKEHKKACVHGGKTYS  
HGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTEYPCRHPEKVAGKCKICPEDKADPGHSE  
ISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLVKDEETEAQRGEVPGPRPH  
SQNLPLDSDQESQEARLPERGTALPTARWPPRRSLERLPSDPGAEGHGQSRQSDQDITKT

**Signal peptide:**

amino acids 1-25

## FIGURE 83

GACAGCTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTGCCCTCGCTACGCAGAGCCTCTCC  
GTGGCTTCCGCACCTTAGCATTAGGCCAGTTCTCTCTCTAATCCATCGTCACCTCTCCTGTCA  
TCCGTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGGCTCTCATGCTCAGTTGGTTCTGACTC  
TCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTGGGCCAGAACAGCCTGTCCAGGCCCTGGTGGGGAG  
GACGCAGCATTCTCTGTTCTGTCTCTAAGACCAATGCAGAGGCCATGGAAGTGCAGTTCTCAGGGG  
CCAGTTCTCTAGCGTGGTCCACCTCTACAGGGACGGGAGGACCAAGGCTTATGAGATGCCACAGTATC  
AAGGCAGGACAAAACTGGTGAAGGATTCTATTGCGGAGGGGCGATCTCTGAGGCTGGAAAACATTACT  
GTGTTGGATGCTGGCCTATGGGTGCAGGATTAGTTCCAGTCTTACTACCAGAACGGCATCTGGAGCT  
ACAGGTGTCAGCACTGGGCTCAGTCCCTCATTTCCATCACGGGATATGTTGATAGAGACATCCAGCTAC  
TCTGTCAGTCCTCGGGCTGGTCCCCGGCCACAGCGAAGTGGAAAGGTCACAAGGACAGGATTGTC  
ACAGACTCCAGGACAAACAGAGACATGCATGGCCTGTTGATGTGGAGATCTCTGACCGTCCAAGAGAA  
CGCCGGGAGCATATCCTGTTCCATGCGGCATGCTCATCTGAGCCGAGGGTGGAAATCCAGGGTACAGATAG  
GAGATACCTTTTCGAGCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAAACTCTGCTGTGGCCTA  
TTTTTGGCATTGTTGACTGAAGATTTCTTCTCAAATTCCAGTGGAAATCCAGGGGAACTGGACTG  
GAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCGGAAACACGCACTGGAGGTGACTCTGGATCCAG  
AGACGGCTCACCGAAGCTCTGCGTTCTGATCTGAAACTGTAACCCATAGAAAGCTCCCCAGGAGGTG  
CCTCACTCTGAGAAGAGATTACAAGGAAGAGTGTGGTGGCTTCTCAGAGTTCCAAGCAGGGAAACATTA  
CTGGGAGGTGGACGGAGGACACAATAAAAGTGGCGCGTGGAGTGTGGGGATGATGTGGACAGGAGGA  
AGGAGTACGTGACTTTGTCTCCCGATCATGGGACTGGGTCTCAGACTGAATGGAGAACATTGTATTC  
ACATTAATCCCGTTTATCAGCGTCTCCCCAGGACCCACCTACAAAATAGGGTCTTCTGACTA  
TGAGTGTGGGACCATCTCTTCTCAACATAAAATGACAGTCCCTTATTTATACCCCTGACATGCGGTTG  
AAGGCTTATTGAGGCCCTACATTGAGTATCCGCTCTATAATGAGCAAAATGGAACATCCCATAGTCATCTGC  
CCAGTCACCCAGGAATCAGAGAAAGAGGCCCTTGGCAAAGGGCTCTGCAATCCCAGAGACAAACAG  
TGAGTCCTCCTCACAGGCAACCACGCCCTCCCTCCCCAGGGTGAATGTAGGATGAATCACATCCCACAT  
TCTTCTTAGGGATATAAGGTCTCTCTCCAGATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCA  
GATGAAGGGGGACTGGCCTGTCCACATGGAGTCAGGTGTCATGGCTGCCCTGAGCTGGAGGAAGAAGG  
CTGACATTACATTAGTTGCTCTCACTCCATCTGCTAAGTGAATCTGAAATACCACCTCAGGTGAAG  
AACCGTCAGGAATTCCCATCTCACAGGCTGTGGTGAAGATAAGTAGACAAGGAATGTGAATAATGCTTAG  
ATCTTATTGATGACAGACTGTATCCTAATGGTTGTCATTATATTACACTTCAGTAAAAAA

## **FIGURE 84**

MAIMLMLSLVLSLLKLGSQWQVFGPDKPVQALVGEDAASFCLSPKTNAEAMEVRFFRGQFSSVVH  
LYRDGKDQPFMQMMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISSQSYYQKAIWELQ  
VSALGSVPPLISITGYVDRDIQLLCQSSGWFPRPTAKWKGPGQGDLSTDRTNRDMHGLFDVEISL  
TVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLFFGIVGLKIFFSK  
FQWKIQAELDWRRKHGQAEELRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAQEVPHSEKRF  
TRKSVVASQSFQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLSPDHGYWVRLNGEHLYFT  
LNPRFISVFPRTPPTKIGVFLDYECGTISFFNINDQSLIYTLTCRFEGLLRPYIEYPSYNEQNGT  
PIVICPVTQESEKEASWQRASAIPETSNSESSSQATTPFLPRGEM

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 239-255

## **FIGURE 85**

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGACATGCTGCTGCTGCTGCCCT  
GCTCTGGGGAGGGAGAGGGCGGAAGGACAGACAGAACAGTAAACTGCTGACGATGCAGAGTTCCGTGA  
CGGTGCAGGAAGGCCGTGTGTCATGTGCCCTGCTCCTCTACCCCTCGCATGGCTGGATT  
TACCCCTGGCCCAGAGTAGTTCATGGCTACTGGTCCGGAAAGGGGCAATACAGACCAGGATGCTCC  
AGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGAGGAGACTCGGGACCGATTCCACCTCCTTG  
GGGACCCACATACCAAGAATTGCACCCCTGAGCATCAGAGATGCCAGAAGAAGTGTGCGGGGAGA  
TACTTCTTCGTATGGAGAAAGGAAGTATAAAATGGATTATAAACATACCGGCTCTGTGAA  
TGTGACAGCCTTGACCCACAGGCCAACATCCTCATCCCAGGCACCCCTGGAGTCGGCTGCC  
AGAACATCTGACCTGCTGTGCCCTGGCCTGTGAGCAGGGACACCCCTATGATCTCCTGGATA  
GGGACCTCCGTGTCCCCCTGGACCCCTCCACCACCCGCTCCTCGGTGCTCACCTCATCCCACA  
GCCCCAGGACCATGGCACCAGCCTCACCTGTCAGAGGTGACCTTCCCTGGGGCCAGCGTGACCACGA  
ACAAGACCGTCCATCTCAACGTGTCCTACCCGCTCAGAACTGACCATGACTGTCTCCAAGGA  
GACGGCACAGTATCCACAGTCTGGAAATGGCTCATCTGTCACTCCCAGAGGGCAGTCT  
GCGCCTGGTCTGTGCAGTTGATGCAGAGTGACAGCATCCCCTGCCAGGCTGAGCTGG  
GAGGCCTGACCCTGTGCCCTCACAGCCCTAAACCCGGGGGTGCTGGAGCTGCCTGGGTGCAC  
CTGAGGGATGCAGCTGAATTCACCTGCAGAGCTCAGAACCCCTCTCGGTCTCAGCAGGTCTACCT  
GAACGTCTCCCTGCAGAGCAAAGCCACATCAGGAGTGACTCAGGGGGGTGCTGGGGAGCTGGAG  
CCACAGCCCTGGTCTCCTGCGTCATCTCGTGTAGTGAGGTCTGCAGGAAGAAA  
TCGGCAAGGCCAGCAGCGGGCGTGGAGATACGGGCATAGAGGATGCAAACGCTGTCAGGGGTT  
AGCCTCTAGGGGCCCCTGACTGAACCTGGCAGAACAGACTCCCAGACCAGCCTCCCCAG  
CTTCTGCCCGCTCCTCAGGGGGAGGAGGAGCTCCAGTATGCATCCCTCAGCTCCAGATGGTG  
AAGCCTTGGACTCGCGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCCACAG  
ATGAGAAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCCTCCAGGAAGGGGAGAAGTCA  
GAGGCTGATTCTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACTATGAATTATG  
TGCAGAGTGAAAAGCACACAGGCTTAGAGTCAAAGTATCTCAAACCTGAATCCACACTGTGCC  
TCCCTTTATTTTTAACTAAAAGACAGACAAATTCTA

## **FIGURE 86**

MLLMLLPLLWGRERAEGQTSKLLTMQSSVTQEGLCVHPCFSYPSHGWIYPGPVHGYWFREG  
ANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLISRDARRSDAGRYFFRMEKGSIKWNY  
KHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCSPWACEQGTPPMISWIGTSVSPLDPSTTRS  
SVLTLIPQPQDHGTSLTCQVTFPGASVTTNKTVHLNVSYPPQNLMTVFQGDGTVSTVLGNSSL  
SLPEGQSLRLVCAVDADSNPPARLSLSWRGLTLCPSQPSNPGVLELPWVHLRDAAEFTCRAQNP  
LGSQQVYLNVSLSQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRSCRKKSARPAAGVGDTGIE  
DANAVRGSASQGPLTEPWAEDSPPDQPPPASARSSVGEGELOYASLSFQMVKPWDSRGQEATDTE  
YSEIKIHR

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 351-370

## **FIGURE 87**

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGTGAAGGAGCTCTGTAC  
CCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGCTGTTTC  
TCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAAACTTACTTCAGGAATGGACCTGT  
TCTTCGCTCCATCTGCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCCTAGTGCATTGA  
TGGCCTGTATTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTCTGTGACATGACCTCTG  
GGGGTGGCGGCTGGACCTGGTGGCCAGCGTGCATGAGAATGACATGCGTGGGAAGTGCACGGTG  
GGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGACGGCAACTGGC  
CAACTACAACACCTTGGATCTGCAGAGGCCAGCGAGCGATGACTACAAGAACCTGGCTACT  
ACGACATCCAGGCCAAGGACCTGGCATCTGGCACGTGCCAATAAGTCCCCATGCAGCACTGG  
AGAAACAGCTCCCTGCTGAGGTACCGCACGGACACTGGCTCCTCCAGACACTGGACATAATCT  
GTTTGGCATCTACCAAGAAATATCCAGTGAAATATGGAGAAGGAAAGTGTGGACTGACAACGCC  
CGGTGATCCCTGTGGCTATGATTTGGCAGGCCAGAAAACAGCATCTTATTACTCACCCAT  
GGCCAGCGGAATTCACTGCGGATTGTTAGTTCACTGAGGTTATTAATAACGAGAGAGCAGCAA  
CGCCTTGTGTGCTGGAATGAGGTACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAG  
GATACTTCCAGAGGCCAGTCCCAGCAGTGTGGAGATTTCTGGTTGATTGGAGTGGATAT  
GGAACATCATGTTGGTTACAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCG  
TTGAGAGTTTGTGGAGGGAAACCCAGACCTCTCCACCAGAGATCCAGGATGGAGAA  
CAACTTACCCAGTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAATCATATTGACTCAAGA  
AAAAAA

## **FIGURE 88**

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTENGVI  
YQTFCDMTSGGGGWTLVASVHENDMRGKCTVGRWSSQQGSKADYPEDGDNWANYNTFGSAEAAT  
SDDYKNPGYYDIQAKDLGIWHVPNPKSPMQHWRNSSLRRTDTGFLQTLGHNLFGIYQKYPVKYG  
EGKCWTNDNGPVIPVYDFGDAQKTASYYSPYQREFTAGFVQFRVFNNEAANALCAGMRVTGCN  
TEHHCIGGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSSREITEAAVLLFYR

**Important features:**

**Signal peptide:**

amino acids 1-16

**N-glycosylation site.**

amino acids 163-167

**Glycosaminoglycan attachment sites.**

amino acids 74-78, 289-293

**N-myristylation sites.**

amino acids 76-82, 115-121, 124-130, 253-259, 292-298

## **FIGURE 89**

CTAGATTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTGAACCTCCAGCCTCAGAGAC  
CGCCGCCCTTGTCCCCGAGGGCCATGGGCCGGTCTCAGGGCTTGTGCCCTCTCGCTTCTGACG  
CTCCTGGCGCATCTGGTGGTGGTCACTCACCTTATTCTGGTCCCAGGACAGAACATACAGGCCTG  
CCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTCAAGCTGGTGGCCGCGCTCT  
CTGTCACCCCTGGGCCTTTGCAGTGGAGCTGGCCGGTTCCCTCTCAGGAGTCTCATGTTAAC  
AGCACCCAGAGCCTCATCTCCATTGGGCTCACTGTAGTGCATCCGTGGCCCTGTCCTTCCAT  
ATTCGAGCGTTGGAGGTGCACTACGTATTGGTACATTTTGCTTCTGCAGTGCCTTCCAGCTG  
TCACTGAAATGGCTTATTCGTCACCGTCTTGGCTGAAAAAGAAACCCCTCTTGATTACCTTCA  
TGACGGAACCTAAGGACGAAGCCTACAGGGCAAGGGCGCTCGTATTCCCTGGAAGAAGGAAG  
GCATAGGCTTCGGTTTCCCTCGAAACTGCTCTGCTGGAGGATATGTGTTGAAATAATTACG  
TCTTGAGTCTGGGATTATCCGATTGTATTAGTGCCTTGTAAATAATGTTTGTAACA  
TTAAGACTTATACAGTTAGGGACAATTAAAAAAAAAA

## **FIGURE 90**

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLGLFA  
VELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFC SALPAVTEMALFV  
TVFGLKKPF

**Transmembrane domain:**

amino acids 12-28 (type II), 51-66, 107-124

## **FIGURE 91**

CTGGGACCCGAAAAGAGAAGGGAGAGCGAGGGACGAGAGCGGAGGAGGAAGATGCAACTGAC  
TCGCTGCTGCTTCGTTCTGGTGCAGGGTAGCCTATCTGGTCACTGTGGCCAGGATGATG  
GTCCTCCGGCTCAGAGGACCTGAGCGTGTGACCAACAGGGCCAGCCCCGGCCCCGGGTGCCT  
CGGAAGCGGGGCCACATCTCACCTAAGTCCGCCCATGGCAATTCCACTCTCCTAGGGCTGCT  
GGCCCCGCTGGGAGGCTTGGGCATTCTGGCAGCCCCCAACGCCGAACCACAGCCCC  
CACCTCAGCCAAGGTGAAGAAAATCTTGGCTGGGCACCTACTCCAACATCAAGACGGTG  
GCCCTGAACCTGCTCGTCACAGGGAAAGATTGTGGACCATGGCAATGGACCTTCAGCGTCCACTT  
CCAACACAATGCCACAGGCCAGGGAAACATCTCATCAGCCTCGTGGCCCCAGTAAAGCTGTAG  
AGTTCCACCAGGAACAGCAGATCTCATCGAAGCCAAGGCCCTCCAAAATCTTCAACTGCCGGATG  
GAGTGGGAGAAGGTAGAACGGGGCCGGACCTCGCTTGCACCCACGACCCAGCCAAGATCTG  
CTCCCGAGACCACGCTCAGAGCTCAGGCCACCTGGAGCTGCTCCAGGCCCTCAAAGTCGTCTGT  
TCTACATCGCCTTCTACAGCACGGACTATCGGCTGGTCCAGAAGGTGTGCCAGATTACAAC  
CATAGTGATACCCCCACTACCCATCTGGGTGACCCGGGGCAGGCCACAGAGGCCAGGGC  
TGGAAGGACAGGCCTGCCATGCAGGAGACCATCTGGACACCGGGCAGGGAAAGGGTTGGG  
AGGCAGGGAGGGGGGTGGAGACGAGGAGATGCCAAGTGGGCCAGGGCAAGTCAAGTGGCAG  
AGAAAGGGTCCAAGTGTGGTCCAAACCTGAAGCTGTGGACTGACTAGATCACAGGAGCACTGG  
AGGAGGAGTGGCTCTGTGCAGCCTCACAGGGCTTGCCACGGGCCACAGAGAGATGCTGG  
TCCCCGAGGCCTGTGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGAGGAAGCTAAC  
CCTTGGTTCTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGAGATTTCATCAGTGTGGACA  
GCCGTCAACTTAGGATGGATGGCTGAGAGGGCTTCTAGGAGCCAGTCAGCAGGGTGGGG  
GCCAGAGGAGCTCCAGCCCTGCCAGTGGCGCCCTGAGCCCCTTGCTGTGCTGAGCATGG  
CATGAGGCTGAAGTGGCAACCTGGGGCTTGTGACAGATTGACCATCTGTCTCCAGC  
CAGGCCACCCCTTCCAAAATCCCTCTGCCAGTACTCCCCCTGTACCAACCCATTGCTGATG  
GCACACCCATCTTAAGCTAACAGACAGGACGATTGTGGCTCCACACTAACGCCACAGCC  
CGCGTGCTGTGTGTCCTCTCCACCCCAACCCCTGCTGGCTCCTGGGAGCATCCATGTCCCG  
GAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTCAGACCGGGGTTCTCCGGATCTGGATGGCG  
CGCCCTCTCAGCAGCGGGCACGGTGGGGGGCCGGCCGCAGAGCATGTGCTGGATCTGTT  
TGTGTGTCTGTCTGTGGTGGGGAGGGAGGGAAAGTCTTGTGAAACCGCTGATTGCTGACTTT  
TGTGTGAAGAATCGTGTCTTGGAGCAGGAAATAAGCTGCCCGGGCA

## **FIGURE 92**

MQLTRCCFVFLVQGSILVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANSTL  
LGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNNGTF  
SVHFQHNATGQGNISISLVPPSKAVEFHQQQIFIEAKASKIFNCRMEWEKVERGRTSLCTHDP  
AKICSRDHAQSSATWSCSQPFKVVVCVYIAFYSTDYRLVQKVPDYNHSDTPYYPSG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-14

**N-glycosylation sites.**

amino acids 62-65, 127-130, 137-140, 143-146

**2-oxo acid dehydrogenases acyltransferase**

amino acids 61-71

## **FIGURE 93**

CGGTGGCCATGACTGCGGCCGTGTTCTCGCTGCGCCTTCATTGCCTCGGGCCTGCGCTGCC  
CTTTATGTCTCACCATGCCATCGAGCCGTTGCGTATCATCTTCCTCATGCCGGAGCTTCTT  
CTGGTTGGTGTCTACTGATTGTCCTTGTGTTGGTTCATGGCAAGAGTCATTATTGACAACA  
AAGATGGACCAACACAGAAATATCTGCTGATCTTGGAGCGTTGTCCTGTCTATATCCAAGAA  
ATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTGAAGAGTATAAACCC  
AGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTCTGGCTTGGCTTGGATCATGA  
GTGGAGTATTTCCCTTGTGAATACCCCTATCTGACTCCCTGGGCCAGGCACAGTGGGCATTCA  
GGAGATTCTCCTCAATTCTCCCTTATTCACTGCTGGCATTATCTGCTGCATGT  
ATTCTGGGCATTGTATTTGATGGCTGTGAGAAGAAAAGTGGGCATCCTCTTATCGTC  
TCCTGACCCACCTGCTGGTGTCAAGCCCAGACCTTCATAAGTTCTTATTATGAAATAACCTGGCG  
TCAGCATTATAATCCTGGTGCATGGCACCTGGCATTCTAGCTGCGGGAGGCAGCTGCCG  
AAGCCTGAAACTCTGCCTGCTGCCAAGACAAGAACTTCTTACAACCAGCGCTCCAGAT  
AACCTCAGGGAACCAAGCACTCCAAACCGCAGACTACATCTTAGAGGAAGCACAACTGTGCCT  
TTTCTGAAAATCCCTTTCTGGTGAATTGAGAAAGAAATAAAACTATGCAGATA

## **FIGURE 94**

MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKDG  
PTQKYLLIFGAFVSVYIQEMFRFAYYKLLKASEGLKSINPGETAPSMRLLAYVSGLGFGIMSGV  
FSFVNTLSDSLGP GTVGIHGDSPQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKW GILLIVLLT  
HLLVSAQTFI SYYGINLASAFI IILVLMGTW AAGGSCRSLKLCLLCQDKNFLLYNQR SR

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domains:**

amino acids 32-51, 119-138, 152-169, 216-235

**Glycosaminoglycan attachment site.**

amino acids 120-123

**Sodium:neurotransmitter symporter family protein**

amino acids 31-65

## **FIGURE 95**

AATTTTCACCAGAGTAAACTTGAGAAACCAACTGGACCTTGAGTATTGTACATTTGCCTCGTG  
GACCCAAAGGTAGCAATCTGAAACATGAGGAGTACGATTCTACTGTTTGTCTTAGGATCAAC  
TCGGTCATTACCACAGCTAAACCTGTTGGACTCCCTCCCACAAAACTGGCTCCGGATCAGG  
GAACACTACCAACCAACAGCAGTCAAATCAGGTCTTCCTTAAAGTCTGATACCATTAAACA  
CAGATGCTCACACTGGGCCAGATCTGCATCTGTTAAATCCTGCTGCAGGAATGACACCTGGTAC  
CCAGACCCACCCATTGACCCCTGGGAGGGTTGAATGTACAACAGCAACTGCACCCACATGTGTTAC  
CAATTTTGTACACAACTTGGAGCCCAGGGCACTATCCTAAGCTCAGAGGAATTGCCACAAATC  
TTCACGAGCCTCATCATCCATTCTTGTTCGGAGGCATCCTGCCACCAGTCAGGCAGGGC  
TAATCCAGATGTCCAGGATGGAAGCCTCCAGCAGGAGGAGCAGGTGTAATCTGCCACCCAGG  
GAACCCCAGCAGGCCCTCCCAACTCCAGTGGCACAGATGACGACTTGCAGTGACCACCCCT  
GCAGGCATCCAAAGGAGCACACATGCCATCGAGGAAGCCACCACAGAATCAGCAAATGGAATTCA  
GTAAGCTGTTCAAATTTCAACTAAGCTGCCTCGAATTGGTGATACTGTGAATCTTATC  
ATTGATTATATTATGGAATAGATTGAGACACATTGGATAGTCTAGAAGAAATTAAATTCTTAATT  
TACCTGAAAATATTCTGAAATTTCAGAAAATATGTTCTATGTAGAGAAATCCAACTTTAAAAAA  
CAATAATTCAATGGATAAAATCTGTCTTGAATATAACATTATGCTGCCTGGATGATATGCATAT  
TAAAACATATTGAAAAACTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 96**

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSSLIPLTQM  
LTLPDILHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTILSSEE  
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG  
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

**Signal peptide:**

amino acids 1-16

## **FIGURE 97**

GCTCAAGTGCCTGCCTTGCCCCACCCAGCCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGCTCT  
CTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGCTGCTTCGCCCCAGGCTCTCCCAAGGCCAGCCTGC  
GTCCCTGCCTGGCTGCTTGTGTCCTCGTCCCCAGGCTCTCCCAAGGCCAGCCTGC  
AGAGCTGTCTGTGAAGTTCAGAAAATGGTGAATTTCCTTATACCTGACCAAGTGC  
CGCTGCCCGTGAGGGGCTGAAGGCCAGATCGTCTGTCAGGGACTCAGGCAAGGCAACTGAG  
GGCCCATTTGCTATGGATCCAGATTCTGGCTTCTGCTGGTACCCAGGGCCCTGGACCGAGAGGA  
GCAGGCAGAGTACCAAGCTACAGTCACCCCTGGAGATGCAGGATGGACATGTCTTGTGGGTCAC  
AGCCTGTGCTTGTGACGTGAAGGATGAGAATGACCAGGTGCCCTTCTCAAGCCATCTAC  
AGAGCTGGCTGAGCCGGGTACCCAGGCCCTGGCATCCCTCTCCTTGAGGCTTCAGACCG  
GGATGAGCCAGGCACAGCCACTCGGATCTCGATTCCACATCTGAGCCAGGCTCCAGGCCAGC  
CTTCCCCAGACATGTTCCAGCTGGAGCCTGGCTGGGCTCTGGCCCTCAGCCCCAAGGGGAGC  
ACCAGCCTGACCACGCCCTGGAGAGGACCTACCAGCTGGTACAGGTCAAGGACATGGGTGA  
CCAGGCCCTAGGCCACCAGGCCACTGCCACCGTGGAGCTCCATCATAGAGGACACTGGGT  
CCCTAGAGCCTATCCACCTGGCAGAGAATCTCAAAGTCTATACCCGACCACATGGCCAGGTA  
CACTGGAGTGGGGTGTATGTGCACTATCACCTGGAGAGCCATCCCCGGGACCCCTTGAAGTGA  
TGCAGAGGGAAACCTCTACGTGACCAGAGAGCTGGACAGAGAAGGCCAGGCTGAGTACCTGCTCC  
AGGTGGGGCTCAGAATTCCATGGCGAGGACTATGCGGCCCCCTGGAGCTGACGTGCTGGT  
ATGGATGAGAATGACAACGTGCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCT  
CAGTCCACCAGGTACTGAAGTGAATAGACTGTCAGCAGAGGATGAGATGCCCGGCTCCCCCA  
ATTCCCACGTTGTATCAGCTCTGAGCCCTGAGCCTGAGGATGGGTAGAGGGAGAGCCTC  
CAGGTGGACCCCACCTCAGGCAGTGTGACGCTGGGGTCTCCCACTCGAGCAGGCCAGAACAT  
CCTGCTCTGGTCTGGCATGGACCTGGCAGGCCAGAGGGTGGCTCAGCAGCACGTGTAAG  
TCGAAGTCGAGTCACAGATATCAATGATCACGCCCTGAGTCAGTCACTTCCAGATTGGGCT  
ATAAGCCTCCCTGAGGATGTGGAGCCGGACTCTGGTGGCATGCTAACAGCCATTGATGCTGA  
CCTCGAGCCCGCCTCCGCTCATGGATTGGCCATTGAGAGGGGAGACACAGAAGGGACTTTG  
GCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAAGAACCTCAGTTATGAG  
GCAGCTCCAAGTCATGAGGTGGTGGTGGTGGCAGAGTGTGGCAAGCTGGTGGGGCAGGCC  
AGGCCCTGGAGCCACCGCCACGGTGAATGTGCTAGTGGCTAGCTGGCAGCCCTGACCATC  
ACCAGGAGAGCTACGAGGCCAGTGTGCTAGCTGGCCATCAGGTTCTCCCTAGTCATGACTCAGAGGGCTGGCT  
CAGCCCTCCGACCCCATCAGCCGAACCCCTCAGGTTCTCCCTAGTCATGACTCAGAGGGCTGGCT  
CTGCATGAGAATCTCCGGGAGGTGACACCCGCCCAGTCACCTGGCCCTGCAAGGGGCCAGCCTGGG  
ACACCTACACGGTGTGGAGGCCAGGATACAGCCCTGACTCTTGCCTGTGCCCTCCAA  
TACCTCTGCAACACCCGCAAGACCATGGCTGATGTCAGTGGACCCAGCAAGGACCCGATCT  
GGCCAGTGGGACGGTCCCTACAGCTTCACTGGTCCCAACCCACGGTCAACGGGATGGC  
GCCTCCAGACTCTAATGGTCCATGCCCTACCTCACCTGGCCCTGCAATTGGTGGAGGCCACGT  
GAACACATAATCCCCGTGGTGGCAGGCCACAATGCCAGATGTGGCAGCTGGTGGCTGAGTGAT  
CGTGTGCGCTGCAACGTGGAGGGCAGTGCATGCGCAAGGTGGGGCGATGAAGGGCATGCCA  
CGAAGCTGTCGGCAGTGGCATCTTGTAGGCACCCCTGGTAGCAATAGGAATCTCCTCATCTC  
ATTTCACCCACTGGACCATGTCAGGAAGAAGGCCGGATCAACCAGCAGCACAGCGTGCCCT  
GAAGGCCAGTGTCTGAATGGCCAGGCAGCTAGCTGGAGCTTGGCCTCTGGCTCCATCTGAG  
TCCCTGGGAGAGGCCAGCACCAAGATCCAGCAGGGACAGGACAGAGTAGAAGCCCCCTCCA  
TCTGCCCTGGGGTGGAGGCACCATCACCACCACTGGGAGCTGTCAGAGCCTGGACACCAACTT  
TATGGACTGCCATGGAGTGTCCAATGTCAGGGTGTGCTTGGCCAATAATAAGCCCCAGAGAA  
CTGGGCTGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAG

## **FIGURE 98**

MVPAWLWLLCVSVPQALPKAQPAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSGKAT  
EGPFAMDPDSGFLLVTRALDREEQAQEYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVPHFSQAI  
YRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPSPDMFQLEPRLGALALSPKG  
STSLDHALERTYQLLVQVKDMGDQASGHQATATVEVSIIESTWVSLPEIHLAENLKVLYPHHMAQ  
VHWSSGGDVHYHLESHPGPFEVNAEGNLYVTRELDREAAQEYLLQVRAQNSHGEDYAAPPLEHVL  
VMDENDNVPICPPRDPPTVSIPELSPPGTEVTRLSAEDADAPGSPNSHVYQLLSPPEPEDGVEGRA  
FQVDPTSGSVTLGVPLRAGQNILLVLAMDLAGEGGSSTCEVEVAVTDINDHAPEFITSQIG  
PISLPEDVEPGTLVAMLTAIDADLEPAFRIMDFAIERGDTEGTFGLDWEPSGHVRLRLCKNLSY  
EAAPSHEVVVVVQSVAKLGVGGPGPGATATVTLVERVMPPKLDQESYEASVPISAPAGSFLLT  
IQPSDPISRTLRFSLVNDSEGWLICIEKFSGEVHTAQSLQGAQPGDTYTVLVEAQDTALTTLAPVPS  
QYLCTPRQDHGLIVSGPSKDPDLASGHGPYSFTLGPNPTVQRDWRQLTNGSHAYLTTLALHWEP  
REHIIPVVVSHNAQMWMQLLVRVIVCRCNVEGQCMRKVGRMKGMPTKLSAVGILVGTIVAIIGIFI  
LIFTHWTMSRKKDQPADSVPLKATV

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 762-784

## **FIGURE 99**

GGCTGACCGTGCTACATTGCCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGTGCCCACGCCCTG  
AGTCCAAGATTCTCCCAGGAACACAAACCTAGGAGACCCACGCTCTGGAAGCACCAGCCTTTA  
TCTCTCACCTCAAGTCCCCTTCTCAAGAATCTCTGTTCTTGCCTCTAAAGTCTTGGTAC  
ATCTAGGACCCAGGCATCTGCTTCCAGCCACAAAGAGACAGATGAAGATGCAGAAAGGAAATG  
TTCTCCTATGTTGGTCTACTATTGCAATTAGAAGCTGCAACAAATTCAATGAGACTAGCACC  
TCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGGCCACAACTCTGGGTCCAG  
TGTGACCTCCAGTGGGTCAAGCACAGCCACCATCTCAGGGTCCAGGTGACCTCCAATGGGTCA  
GCATAGTCACCAACTCTGAGTCCATACAACCTCCAGTGGGATCAGCACAGGCCACAACTCTGAG  
TTCAGCACAGCCTCAGTGGGATCAGCATAGCCACAACTCTGAGTCCAGCACACCTCCAGTGG  
GGCCAGCACGCCACCAACTCTGAGTCCAGCACACCCCTCCAGTGGGCCAGCACAGTCACCAACT  
CTGGGTCCAGTGTGACCTCCAGTGGAGCCAGCACTGCCACCAAACCTCTGAGTCCAGCACAGTGCC  
AGTAGGGCCAGCACTGCCACCAAACCTCTGAGTCTAGCACACTCTCCAGTGGGCCAGCACAGCCAC  
CAACTCTGACTCCAGCACAAACCTCCAGTGGGCTAGCACAGGCCACCAACTCTGAGTCCAGCACAA  
CCTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACT  
GCCACCAACTCTGAGTCCAGCACAAACCTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAG  
AACGACCTCCAATGGGCTGGCACAGCCACCAACTCTGAGTCCAGCACAGCACCTCCAGTGGGCCA  
GCACAGCCACCAACTCTGACTCCAGCACAGTGTCCAGTGGGCCAGCACTGCCACCAACTCTGAG  
TCCAGCACGACCTCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGG  
GGCTAGCACGCCACCAACTCTGACTCCAGCACAAACCTCCAGTGGGCCAGCACAGCCACCAACT  
CTGAGTCCAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACACCCCTCC  
AGTAGGGCCAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGCCACACAGCCAC  
CAACTCTGAGTCCAGCACAGTGTCCAGTGGGCCAGCACTGCCACCAAACCTCTGAGTCCAGCACAA  
CCTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAAACCTCCAGTGGGCCAGCAC  
GCCACCAACTCTGACTCCAGCACAAACCTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCTAG  
CACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACAAACCTCCAGTGGGCCA  
ACACAGCCACCAACTCTGGTCCAGTGTGACCTCTGCAGGCTCTGGAACAGCAGCTCTGACTTGA  
ATGCACACAACCTTCCCATAGTGCATCTACTGCAGTGAAGTGGAGAAAGCCTGGTGGTCCCTGGT  
GCCGTGGAAATCTCCTCATACCCCTGGTCTCGGTTGCGGCCGTGGCTTGTGGCTTGTGGC  
TCTTCTCTGTGAGAAACAGCCTGCTGGTCAAGGCCCTGGAGGGAAATCATGGAGCCCCACAGGCCAG  
GTGGAGTCTTAAGTGGTCTGGAGGAGACAGTATCGATAGCAGTGGAGATGAGCGGGAGGA  
ACAGCGGGCCCTGAGCAGCCCCGGAAAGCAAGTGCAGCATTCTCAGGAAGGAAGAGACCTGGCA  
CCCAAGACCTGGTTCTCCTTCAATTCACTCCAGGAGACCCCTCCAGCTTGTGAGATCCTGAA  
AATCTGAAAGAAGGTATTCTCACCTTCTGCTTACAGACACTGGAAAGAGAAATACTATAT  
TGCTCATTAGCTAAGAAATAATACATCTCATCTAACACACAGACAAAGAGAAAGCTGTGCTTG  
CCCCGGGGTGGGTATCTAGCTGAGATGAACCTAGTTAGGAGAAACCTCCATGCTGGACTC  
CATCTGGCATTCAAATCTCACAGTAAAATCAAAGACCTCAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 100**

MKMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATISGS  
SVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSESSTPSS  
GASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSSTTSSGASTA  
TNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTTSNGAGTATNSES  
STTSSGASTATNDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSSGASTATNDSSTTSS  
GAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGANTATNSESSTVSSGASTA  
TNSESSTTSSGVSTATNSESSTTSSGASTATNDSSTSSEASTATNSESSTVSSGISTVTNSES  
STTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGSLVPWEIFLITLVSVA  
AVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGPGPGGNHGAPHRPRWSPNWFWRPVS  
AMEMSGRNSGP

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 510-532

## **FIGURE 101**

GGCCGGACGCCCTCCCGTTACGGGATGAATTAAACGGCGGTTCCGCACGGAGGTGTGACCCCTA  
CGGAGCCCCAGCTGCCACGCACCCACTCGCGTCGCGCGTGCCTGCTGTACAGGTG  
GGAGGCTGGAACTATCAGGCTGAAAAACAGAGTGGTACTCTCTGGAAAGCTGGCAACAAAT  
GGATGATGTGATAATGCATTCCAGGGAAAGGGAAATTGTGGTGCTCTGAACCCATGGTCAATT  
AACGAGGCAGTTCTAGCTACTGCACGTACTTCATAAAGCAGGACTCTAAAGCTTGGAAATCAT  
GGTGTCAGGAAAGGGATTTACTTTACTGACTCTGTTGGGAAGCTTTGGAAAGCATT  
TCATGCTGAGTCCCTTTTACCTTGATGTTGAAACCCATCTGGTATCGCTGGATCAACAAAC  
CGCCTTGTGGCAACATGGCTCACCTACCTGTGGCATTATTGGAGACCATGTTGGTGTAAAGT  
GATTATAACTGGGATGCATTGTCCTGGAGAAAGAAGTGTCAATTATCATGAACCATCGGACAA  
GAATGGACTGGATGTTCTGTGGAATTGCGATAGCTACCTCAGATTGGAGAAAATT  
TGCCTCAAAGCGAGTCTCAAAGGTGTTGGATTGGTGGCCATGCAGGCTGCTGCCTATAT  
CTTCATTCAAGGAAATGGAAGGATGACAAGAGCCATTGAAAGACATGATTGATTACTTTGT  
ATATTCAACGAACCACTCAACTCCTCATATCCCAGAAGGGACTGATCTCACAGAAAACAGCAAG  
TCTCGAAGTAATGCATTGCTGAAAAAAATGGACTTCAGAAATATGAATATGTTTACATCCAAG  
AACTACAGGCTTACTTGTGGTAGACCGTCTAAGAGAAGGTAAGAACCTTGATGCTGTCCATG  
ATATCACTGTGGGTATCCTCACAAACATTCTCAATCAGAGAAGCACCTCCTCCAAGGAGACTT  
CCCAGGGAAATCCACTTCACGTCACCGGTATCCAATAGACACCCCTCCCCACATCCAAGGAGGA  
CCTTCAACTCTGGTGCCACAAACGGTGGGAAGAGAAGAAGAGGCTGCGTCCCTATCAAG  
GGGAGAAGAATTTTATTACCGGACAGAGTGTCAATTCCACCTTGAAGTCTGAACCTCAGGGTC  
CTTGTGGTCAAATTGCTCTATACTGTATTGGACCTGTCAGCCCTGCAATGTGCCTACTCAT  
ATATTGTACAGTCTGTTAAGTGGTATTATAATCACCATTGAATCTTGCTGCAAGAGA  
GAATATTGGTGGACTGGAGATCATAGAACATTGCAATTGACTTTACACAAACAGCCACAT  
TTAAATTCAAAGAAAATGAGTAAGATTAAAGGTTGCCATGTGAAAACCTAGAGCATATTG  
GAAATGTTCTAAACCTTCTAACGTCAGATGCATTGCAATTGACTATGCGAATATTCTACT  
GCCATATTGTTAAAGATATTGCACTTAATTGCTGGGAAAATATTGCTACAATT  
TTAATCTCTGAATGTAATTGATACTGTCAGATAGCAGGGAGTGATGGGGTGAATAACTT  
GGGCCAGAATATTAAACAAATCATCAGGCTTTAAA

## **FIGURE 102**

MHSRGREIVVLLNPWSINEAVSSYCTYFIKQDSKSFGIMVSWKGIYFILTLFWGSFFGSIFMLSP  
FLPLMFVNPSWYRWINNRLVATWLTPVALLETMFGVKVIITGDAFVPGERSVIIMNHRTRMDWM  
FLWNCLMRYSLRLEKICLKASLKGVPFGFWAMQAAAYIFIHRKWKKSHFEDMIDYFCDIHEP  
LQLLIFPEGTDLTENSRSNAFAEKNGLQKYEYVLHPRTTGFTFVVDRLREGKNLDAVHDITVA  
YPHNIPQSEKHLLQGDFPREIHFHVRYPIDTLPTSKEDLQLWCHKRWEEKERLRSFYQGEKNF  
YFTGQSVIPPCKSELRVLVVKLLSILYWTLFSPAMCLLIYLYSLVKWYFIITIVIFVLQERIFGG  
LEIIELACYRLLHKQPHLNSKKNE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domains:**

amino acids 44-63, 90-108, 354-377

## **FIGURE 103**

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCTGCGCCTGAGACAGCTGGCCTGACC  
TCCAAATCATCCATCCACCCCTGCTGTCATCTGTTCTAGTGTGAGATCAACCCACAGGAATA  
TCCATGGCTTTGTCATTTGGTTCTCAGTTCTACGAGCTGGTGTAGGACAGTGGCAAGT  
CACTGGACCGGGCAAGTTGTCAGGGCTTGGTGGGGAGGACGCCGTGTTCTGCTCCCTCT  
TTCCGTGAGACAGTGCAGAGGCTATGGAAGTGCAGGTTCTCAGGAATCAGTTCCATGCTGTGGTC  
CACCTCTACAGAGATGGGGAAAGACTGGGAATCTAAGCAGATGCCACAGTATCGAGGGAGAACTGA  
GTTTGTGAAGGACTCCATTGCAGGGGGCGTGTCTCTAAGGCTAAAAAACATCACTCCCTCGG  
ACATCGCCTGTATGGGTGCTGGTTCAAGTCCCAGATTACGATGAGGAGGCCACCTGGGAGCTG  
CGGGTGCAGCACTGGGCTCACTTCCCTCATTTCCATCGTGGGATATGTTGACGGAGGTATCCA  
GTTACTCTGCTGTCTCAGGCTGGTCCCCAGGCCACAGCCAAGTGGAAAGGTCCACAAGGAC  
AGGATTGTCAGACTCCAGAGCAAATGCAGATGGGTACAGCCTGTATGATGTTGGAGATCTCC  
ATTATAGTCCAGGAAAATGCTGGGAGCATATTGTTCCATCCACCTTGCTGAGCAGAGTCATGA  
GGTGAATCCAAGGTATTGATAGGAGAGACGTTTCCAGCCCTCACCTGGCCTGGCTTCTA  
TTTACTCGGGTTACTCTGTTGCCCTGTTGATGGGATGATAATTGTTCTTC  
AAATCCAAAGGAAAATCCAGGGCAACTGGACTGGAGAAGAAAGCACGGACAGGCAGAAATTGAG  
AGACGCCGGAAACAGCAGTGGAGGTGACTCTGGATCCAGAGACGGCTACCCGAAGCTCTGCC  
TTTCTGATCTGAAACTGTAACCATAGAAAAGCTCCCCAGGAGGTGCTCACTCTGAGAAGAGA  
TTTACAAGGAAGAGTGTGGTGGCTTCAGGGTTCCAAGCAGGGAGACATTACTGGGAGGTGGA  
CGTGGGACAAATGTAGGGTGGTATGTTGGAGTGTGTCGGGATGACGTAGACAGGGGAAACA  
ATGTGACTTGTCTCCAAACAATGGGTATTGGTCTCAGACTGACAACAGAACATTGTT  
ACATTCAATCCCCATTATCAGCCTCCCCCAGCACCCCTCTACACGAGTAGGGGTCTTCT  
GGACTATGAGGGTGGGACCATCTCCTCTCAATACAATGACCAGTCCCTTATTATACCTG  
TGACATGTCAGTTGAAGGCTTGTGAGACCCATATCCAGCATGCCATGATGACGGAGGAAAG  
GGGACTCCCATATTCAATGTCAGTGTCTGGGGATGAGACAGAGAACACCTGCTTAAAGGGC  
CCCACACCACAGACCCAGACACGCCAAGGGAGAGTGTCTCCAGGCTGGCCCCAGCTCT  
CCGGAGCCTGCGCACAGAGAGTCACGCCCTACTCTCTTAGGGAGCTGAGGTTCTGCCCC  
TGAGCCCTGCGAGCAGGGCAGTCACAGCTTCCAGATGAGGGGGATGGCCTGACCTGTGGGAG  
TCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCACATTAGGTTAGTTGTGAAAA  
CTCCATCCAGCTAACGATCTTGAACAAGTCACAACCTCCAGGCTCTCATTTGCTAGTCACGG  
ACAGTGATTCTGCTCACAGGTGAAGGATAAAGAGAACAGAACATGTGAATCATGCTTGCAGGTT  
TGAGGGCACAGTGTGCTAATGATGTTTATATTACATTTCCACCATAAACTCTGTT  
TGCTTATTCCACATTAATTACTTTCTCTATACCAAAATCACCCATGGAATAGTTATTGAAACACC  
TGCTTGTGAGGCTAAAGAATAAGAGGGAGGTAGGATTTTCACTGATTCTATAAGCCCAGCAT  
TACCTGATACCAAAACAGGCAAAAGAAAAACAGAAGAAGGAAACTACAGGTCCATATCC  
CTCATTAAACAGACACAAAAATTCTAAATAAAATTAAACAAAATTAAACTAACAAATATATTTA  
AAGATGATATATAACTACTCAGTGTGGTTGTCACAAATGCAGAGTTGGTTAATATTTAAAT  
ATCAACCAGTGTAAATTCAAGCACATTAATAAGTAAAAAGAAAACCATAAAAAAAA

## **FIGURE 104**

MAFVLILVLSFYELVSGQWQVTGPGKVFQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHAVH  
LYRDGEDWESKQMPQYRGRTEFKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEATWELR  
VAALGSLPLISIVGYVDGGIQLLCCLSSGWFQPTAKWKGPQGQDLSSDSRANADGYSLYDVEISI  
IVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCALCGVVMGMIIVFFK  
SKGKIQAELDWRRKHGQAEELRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAPQEVPHSEKRF  
TRKSVVASQGFQAGRHYWEVDVGQNVGVYVGCRDDVDRGKNNVTLSPNNGYWVRLLTTEHYFT  
FNPHFISLPPSTPPTRGVFLDYEGGTISFFNTNDQSLIYTLLTCQFEGLLRPYIQHAMYDEEKG  
TPIFICPVSWG

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 131-150, 235-259

## **FIGURE 105**

CCTTCACAGGACTCTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTAGGGCTAGGAAAAGAG  
TTTGGTGGGAACCTGGGTTATCGGCCCTCGTCATCTTCATATCCCTGATTGTCCTGGCAGTGTGCATTGGA  
CTCACTGTTCATTATGTGAGATATAATCAAAGAACCTACAATTACTATAGCACATTGTCATTACAC  
TGACAAACTATATGCTGAGTTGGCAGAGAGGCTCTAACAAATTACAGAAATGAGCCAGAGACTTGAAT  
CAATGGTGAAGGATTCATTATGAGATGAGGAGGCTCTAACAAATTACAGAAATGAGCCAGAGACTTGAAT  
AGTCACAGAACGATGGAGTGTGGCTCATATGCTGTTGATTGAGATTTCACTCTACTGAGGATCCTGA  
AACTGTAGATAAAATTGTTCAACTTGTACATGAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTAG  
ATCCTCACTCAGTAAATTAAAAATCAACAAGACAGAACAGACAGCTATCTAAACCATTGCTGCCGA  
ACACGAAGAACGATGGAGTGTGGCTCATATGCTGTTGATTGAGATTTCACTCTACTGAGGATCCTGA  
GCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGTGGAGCAACCTTAATTATGCCACATGGC  
TTGTGAGTGTGCTCACTGTTACAACATATAAGAACCCCTGCCAGATGGACTGCTTCCTTGGAGTAACA  
ATAAAACCTTCGAAATGAAACGGGGTCTCCGGAGAAATAATTGTCATGAAAATACAAACACCCATCACA  
TGACTATGATATTCCTTGAGAGCTTCTAGCCCTGTTACACAAATGCACTAGATAGAGTTGTC  
TCCCTGATGCATCCTATGAGTTCAACCAGGTGATGATGTTGTGACAGGATTGGAGCACTGAAAAT  
GATGGTTACAGTCAAAATCATCTCGACAAGCACAGGTGACTCTCATAGACGCTACAATTGCAATGAACC  
TCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGCTGGCTCCTAGAAGGAAAACAGATGCAT  
GCCAGGGTGAICTGGAGGACCACTGGTAGTTAGCTAGATGCTAGAGATATCTGGTACCTGCTGGAATAGTG  
AGCTGGGGAGATGAATGTGCGAACCAACAAGCCTGGTTTATAGAGTTACGGCCTGGGGACTG  
GATTACTTCAAAACTGGTATCTAAGAGACAAAAGCCTCATGGAACAGATAACATTTTTTGTTGTTTG  
GGTGTGGAGGCCATTAGAGATACAGAAATTGAGAAGACTTGCAAAACAGCTAGATTGACTGATCTCA  
ATAAAACTGTTGCTGATGCATGTTCTTCCAGCTGTTCCGCACGTAAGCATCCTGCTTCTGCCA  
GATCAACTCTGTCATCTGTGAGCAATAGTTGAAACTTATGTCATAGAGAAATAGATAACAAATTAC  
ATTACAGCCTGATTCTCATTTGTTCTAGAAGTTGTCAGAATTGACTTGTGACATAATTGTAAT  
GCATATATAACAAATTGAGCAACTCCTTTCTCAGTTCCGCACGTAAGCATCCTGCTTCTGCCA  
TCAAGGTGAGAACAAAGGAGTGAAGAAAATAAGAAGAAAAAAACCCCTACATTATTGGCACAGAA  
AAGTATTAGGTGTTCTTAGGAAATTAGAAATGATCATATTCAATTGAAAGCTCAAGCAAAGACA  
GCAGAACATCAACTCATTTAGGAAGTATGGAACTAAGTTAGGAAGTCCAGAAAGAACGCAAG  
ATATATCCTTATTTCATTTCAACAAACTACTATGATAATGTAAGAAGATTGTTCTGACCT  
ATAATAATTATACAAACTTCATGCAATGTAATTGTTCTAAGCAAATTAAAGCAAATTATTAAACATTG  
TTACTGAGGATGTCAACATATAACAATAAAATATAACACCA

## **FIGURE 106**

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTvhYvRyNQKKTNYySTLSFTTDKLY  
AEFGREASNNFTEMSRLESMVKNAYKSPLREEFVKSQVIKFQQKHGVLAHMLLICRFHSTED  
PETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQSLRIVGG  
TEVEEGEWPWQASLQWDGSHRCGATLINATWLVAHCFTTYKNPARWTASFGVTIKPSKMKRGL  
RRIIVHEKYKHPHSDYDISLAELSSPVYTNAVHRVCLPDASYEFQPGDVMFVTGFGALKNDGYS  
QNHLRQAQVTLIDATTNEPQAYNDAITPRMLCAGSLEGKTDACQGDGGPLVSSDARDIWYLAG  
IVSWGDECAPKPGVYTRVTALRDWITSKTGI

**Transmembrane domain:**

amino acids 21-40 (type II)

## **FIGURE 107**

AGAGAAAAGAACGCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCGCGAAGAAGTTCCCTG  
CCCCGATGAGCCCCCGCGTCCGCTCCCGACTATCCCAGGCAGGCGTGGGGCACCGGGCCAGC  
GCCGACGATCGCTGCCGTTTGCCTTGGAGTAGGATGTGGTGAAGGATGGGGCTTCTCCCT  
ACGGGGCTCACAATGGCCAGAGAAAGATTCCGTGAAGTGTCTGCGCTGCCTACGCCCTCAA  
TCTGCTCTTGGTTAATGTCCATCAGTGTGGCAGTTCTGCTGGATGAGGGACTACCTAA  
ATAATGTTCTCACTTAACTCAGAACAGAGGGTAGAGGAAGCAGTCATTGACTTACCTTCT  
GTGGTTCATCCGGTCACTGATTGCTGTTGCTTCTTATCATTGTTGGGATGTTAGGATATTG  
TGGAAACGGTAAAAGAAATCTGTTGCTTCTGCTGGTACTTTGGAAAGTTGCTGTCACTTCT  
GTGAGAACTGGCTGTGGCAGGGACATATGAACAGGAACCTATGGTCCAGTACAATGGTCA  
GATATGGTCACTTGAAGGCCAGGATGACAAATTATGGATTACCTAGATATCGGGGCTTACTCA  
TGCTTGAATTTCAGAGAGGTTAACGTGTGGAGTATATTCACTGACTGGTGG  
AAATGACAGAGATGGACTGGCCCCAGATCCCTGCTGTAGAATTCCAGGATGTTCCAAA  
CAGGCCAACAGGAAGATCTCAGTGCACCTTATCAAGAGGGTGTGGGAAGAAAATGATTCCCT  
TTTGAGAGGAACCAAACAACGTGCAGGTGCTGAGGTTCTGGAACTTCGATTGGGTGACACAAA  
TCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTGTATTATGATAGAAGGGAGCCTGG  
ACAGACCAAATGATGTCCTTGAAGAATGACAACCTCAGCACCTGTCATGTCCTCAGTAGAACT  
GTTGAAACCAAGCCTGTCAAGAATCTTGAACACACATCCATGGCAACAGCTTAATACACACT  
TTGAGATGGAGGAGTTAAAAAGAAATGTCACAGAAGAAAACCACAAACTTGTATTGGACT  
TGTGAATTGGAGTACATACTATGTGTTTCAAGAAATATGTAGAAATAAAATGTTGCCATAAAA  
TAACACCTAACGATATACTATTCTATGCTTAAAATGAGGATGAAAAGTTTCATGTCATAAGTC  
ACCACCTGGACAATAATTGATGCCCTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCC  
TGTGTATGACTTTACTGAACACAGTTATGTTGAGGCAGCATGGTTGATTAGCATTCGCA  
TCCATGCAAACGAGTCACATATGGTGGACTGGAGCCATAGTAAAGGGTGTATTACTTCAACAA  
CTAGTATATAAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTATTAA  
CTCAGCGATCTATTCTCTGATGCTAAATAATTATATCAGAAAACCTTCAATATTGGTACT  
ACCTAAATGTGATTGGTGGTTACTAAAATATTCTTACACTAAAAGAGCAAGCTAACACAT  
TGTCTTAAGCTGATCAGGGATTGGTATATAAGCTGTGTTAAATCTGTATAATTCACTGCGAT  
TTCAGTTCTGATAATGTTAAGAATAACCATATTGAAAAGGAAATTGTCCTGTATAGCATCATT  
ATTGGTATTGGCTTCTGTTAATAAGCTTACTATTCTGCTGGCTTATATTACACATATAAC  
TGTTATTAAATACCTAACACTAATTGGAAAATTACAGTGTGATACATAGGAATCATTATC  
AGAATGTAGTCTGGTCTTAGGAAGTTAAATAAGAAAATTGACACATAACTTAGTTGATTCAA  
AAGGACTTGATGCTGTTTCTCCAAATGAAGACTCTTGTGACACTAAACACTTTTAAAAA  
GCTTATCTTGCTCTCCAAAGAAGCAATAGTCTCCAAGTCATATAAAATTCTACAGAAAAA  
TAGTGTCTTTCTCCAGAAAATGCTGTGAGAATCATTAAACATGTGACAATTAGAGATT  
CTTGTTTATTCACTGATTATAACTGTGGCAAATTACAGATTATTAATTTTACAA  
GAGTATAGTATATTATTGAAATGGAAAAGTCATTTACTGTATTGTGTTATTGTTAT  
TTCTCAGAATATGAAAGAAAATTAAATGTGTCATAAAATATTCTAGAGAGTAA

## **FIGURE 108**

MAREDSVKCLRCLLYALNLLFWIIMSISVLAWSAWMRDYLNNVLTLTAETRVEEAVILTYFPVVHP  
VMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWSDMVT  
LKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDSCCVREFPGCSKQAHQ  
EDLSDLYQEGCGKKMYSFLRGTKQLQVLRFGLSIGVTQILAMILTITLLWALYYDRREPGTDQM  
MSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

**Signal peptide:**

amino acids 1-33

**Transmembrane domains:**

amino acids 12-35, 57-86, 94-114, 226-248

## **FIGURE 109**

CCAAGGCCAGAGCTGTGGACACCTTATCCCACCTCATCCTCATCCTCTTCTGTATAAGCCCCTACCACTGCT  
GATAAAGTCTTCTCGTGAGAGCCTAGAGGCCCTTAAAAAAAAACTGCTTGAAGAGAAGGGACAAAGGAACA  
CCAGTATTAAAGAGGATTTCCAGTGTTCAGTGGCAGTGGTCCAGAAGGATGCCTCCATTCCTCTCACCTG  
CCTCTCATCACAGGCACCTCCGTGTCAACCGTGGCCTAGATCCTGTCTGCTTACATCAGCCTGAATGAGC  
CCTGGAGGAACACTGACCACCACTGGATGAGTCAGGTCTCTCTATGTGACAACCATGTGAATGGGAG  
TGGTACCACTTCACGGCATGGCGGAGATGCCATGCCTACCTCTGCATACAGAAAACCACTGTGGAACCC  
CGCACCTGTGGCTCAATGGCAGCCACCCCTAGAAGGCAGGGATTGTGCAACGCCAGGTTGTGCCAGCT  
TCAATGGAACTGCTGTCTGGAACACACCGTGGAAAGTCAAGGTTGCCCTGGAGGCTACTATGTGTATCGT  
CTGACCAAGCCCAGCGCTGCTTCCACGTCTACTGTGGTCATTATGACATCTGCGACGAGGACTGCCATGG  
CAGTGTCAAGATACCAGCGAGTGCACATGCCTCCAGGAACGTGCTAGGCCAGGACATGCTTG  
ATGAAAATGAATGTGAGCAAAACACGGTGGCTGCAGTGAGATCTGTGTGAACCTCAAAACTCCTACCGCTGT  
GAGTGTGGGTTGGCCGTGTGCTAAGAAGTGTGCAAGACTTGTGAAGACGTTGAAGGATGCCACAATAACAA  
TGGTGGCTGCAGCCACTTGTGCTTGGATCTGAGAAAAGGCTACCACTGTGAATGTCCCCGGGCCTGGTGT  
CTGAGGATAACCACACTTGCCAAGTCCCTGTGTTGTGCAATCAAATGCCATTGAAGTGAACATCCCCAGGGAG  
CTGTTGGTGGCCTGGAGCTTCTGACCAACACCTCTGCCAGGGAGTGTCAACGGCACCCATGTCAACAT  
CCTCTCTCTCAAGACATGTGGTACAGTGGTCACTGTGGTAATGACAAGATTGTGCCAGCAACCTCGTGA  
CAGGTCTACCCAAGCAGACCCCCGGGAGCAGGGGACTCATCATCGAACAGCAAGCTGCTGATCCCCGT  
ACCTGCGAGTTCCACGCCGTACACCATTCTGAAGGATACGTTCCAACCTTCGAAACTCCCCACTGAAAT  
CATGAGCCGAAATCATGGGATCTTCCCACTCTGGAGATCTTCAAGGACAATGAGTTGAAGAGCCTTAC  
GGGAAGCTCTGCCACCCCAAGCTCGTGAACCTCTACTTGGCATTGAGCCGTGGTGCACGTGAGCGGC  
TTGGAAGCTTGGTGGAGAGCTGCTTGCACCCACCTCCAGATCGACGAGGTCTGAAATACTACCTCAT  
CCGGGATGGCTGTTCAAGTTGTGGCAAAGACCACAAGGAAGTGTCTGCACTGCCGGTTCTGTCTGGAGTG  
TCCCTGTCTCAAGTTGTGGCAAAGACCACAAGGAAGTGTCTGCACTGCCGGTTCTGTCTGGAGTG  
TTGGACGAGCGTCTCCGCTGTCCCCAGGGTGCACCCGGCAATGCCGTGCTGGGAGGAGAGGACTCAGC  
CGGTCTACAGGGCCAGCCTAACAGGCGGCCGATCCGCATCAGCTGGAGGACTAGTTCGTAGCCATACCTC  
GAGTCCCTGCATTGGACGGCTCTGCTCTTGGAGCTCTCCCCCACCGCCCTCAAGAACATCTGCCAACAGC  
TGGGTTAGACTTCACACTGTGACTCAGACTCCACGACCAACTCACTCTGATTCTGGTCAATTCAAGTGGCA  
CAGGTACAGCACTGCTGAACAATGTGGCCTGGGTGGGTTCATCTTCTAGGGTTGAAAACACTAAACTGTCCA  
CCCAGAAAGACACTACCCCAATTCCCTCATTTCCACTACCTAAACACGTGTATGGTGAATCAGAC  
CACAAAATCAGAAGCTGGGTATAATATTCAAGTACAAACCCATAGAAAAATTAACAGTTACTGAAATTATGA  
CTTAAATACCAATGACTCCTAAATATGTAATAGTTACCTTGAAATTCAATTCAAATGCAGACTAA  
TTATAGGAATTGGAAGTGTATCAATAACAGTATATAATT

## **FIGURE 110**

MPPFLLLTCLFITGTSVSPVALDPCSAIISLNEPWRNTDHQILDESQGPPLCDNHVNGEWYHFTGMAGDAMP  
TFCIPENHCGTHAPVWLNGSHPLEGDGIVQRQACASFNGNCCLWNTTVEVKACPGGYYVYRLTKPSVCFHV  
YCGHFYDICDEDCHGSCDTSECTCAPGTVLGPDRQTCFDENECEQNNGGCSEICVNLKNSYRCECGVGRV  
LRSRGKTCEDVEGCHNNNGGSHSCLGSEKGYQCECPRLVLSEDNHTCQVPVLCKSNAIEVNIPRELVGG  
LELFFLTNTSCRGVSNGTHVNILFSLKTCGTVVDDVNDKIVASNLVTGLPKQTPGSSGDFIIRTSKLLIPVT  
CEFPPRLYTISEGYVPNLRNSPLEIMSRNHGIFPFTLEIFKDNEFEEPYREALPTLKLRSLSYFGIEPVVHV  
SGLESLVESCATPTSKIDEVLKYYLIRDGCVSDDSVKQYTSRDHLAKHFQVPVFKFVGKDHKEVFLHCRV  
LVCGVLDERSRCAQGCHRRMRRGAGGEDSAGLQGQTLTGGPIRIDWED

**Important features of the protein:**

**Signal peptide:**

amino acids 1-16

**N-glycosylation sites.**

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

**Tyrosine kinase phosphorylation sites.**

amino acids 411-418, 443-451

**N-myristoylation sites.**

amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,  
522-528, 531-537

**Aspartic acid and asparagine hydroxylation site.**

amino acids 197-209

**ZP domain proteins.**

amino acids 431-457

**Calcium-binding EGF-like proteins.**

amino acids 191-212, 232-253

## **FIGURE 111**

GAGAGAGGCAGCAGCTGCTCAGGGACAAGGATGCTGGCGTGAGGGACCAAGGCCTGCCCTGCACACTGG  
GCCTCCTCCAGCCAGTGCCTGACCAGGGACTTCTGACCTGCTGCCAGCCAGGACCTGTGTGGGAGGCCT  
CCTGCTGCCCTGGGGTGAACAATCTCAGCTCCAGGCTACAGGGAGACCGGGAGGATCACAGAGCCAGCATGT  
TACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCGATGTC~~AAACCC~~CTGCGCAAACCCGTATCCCC  
ATGGAGACCTTCAGAAAGTGGGATCCCCATCATCATAGCACTACTGAGCCTGGCAGAGTATCATCATIGT  
GGTTGTCCCTCATCAAGGTATTCTGGATAAAACTACTTCCTCTGCCGGCAGCCTCTCCACTTCATCCGA  
GGAAGCAGCTGTGTGACGGAGAGCTGGACTGTCCCTGGGGAGGACGAGGAGCAGTGTCAAGAGCTC  
CCCGAAGGGCCTGCAGTGGCAGTCGCCTCTCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCAC  
AGGGAACTGGTTCTCTGCCCTGTTGACAACACTTCACAGAAGCTCGCTGAGACAGCCTGTAGGCAGATGG  
GCTACAGCAGAGCTGTGGAGATTGCCAGACCAAGGATCTGGATGTTGAAATCACAGAAAACAGCCAG  
GAGCTTGCATGCGGAACCTCAAGTGGCCCTGTCAGGCTCAGGCTCTGGTCTCCCTGCACTGTCITGCC  
TGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGGAGGAGGAGGCTCTGTGGATTCTGGCCTTGGCAGG  
TCAGCATCCAGTACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGCCTCACGGCA  
GCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGGGGCAGGCTCAGACAAACTGGCAG  
CTTCCCATCCCTGGCTGTGGCAAGATCATCATCATTGAATTCAACCCATGTACCCAAAGACAATGACA  
TCGCCCTCATGAAGCTGCAGTCCCACTCACTTCTCAGGCACAGTCAGGCCATCTGTCTGCCCTTCTT  
GATGAGGAGCTCACTCCAGGCCACCCACTCTGGATCATTGGATGGGCTTACGAAGCAGAATGGAGGGAA  
GATGTCAGACATACTGCTGCAGGCGTCAGTCAGGCTATTGACAGCACACGGTGCAATGCGACAGCAG  
ACCAGGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGGAAGGGGTGTGGACACCTGCCAGGG  
GACAGTGGTGGGCCCTGATGTAACCAATCTGACCAAGTCTCAGCCTATCTCAACTGGATCTACAATGTCT  
CTGCCGGGGCCCGAGCACCCAGGAGTATACACCAAGGCTCAGCCTATCTCAACTGGATCTACAATGTCT  
GGAAGGCTGAGCTGTAATGCTGCTGCCCTTGCAGTGCCTGGAGCCCTCCCTGCCCTGCCACCT  
GGGATCCCCAAAGTCAGACACAGAGCAAGAGTCCCTGGTACACCCCTCTGCCACAGCCTCAGCAT  
TTCTGGAGCAGCAAAGGCCCTCAATTCCCTGTAAGAGACCCCTCGCAGCCAGGGCGCCAGAGGAAGTCA  
GCAGCCCTAGCTGCCACACTTGGTGCCTCAGCATCCCAGGGAGAGACACAGCCACTGAACAAGGTCT  
CAGGGGTATTGCTAAGCCAAGAAGGAACCTTCCCACACTGAAATGGAAGCAGGCTGTCTGTAAAAGCC  
CAGATCACTGTGGCTGGAGAGGAGAAGGAAAGGGTCTGCCAGCCCTGCGCTTCAACCATCCCCAA  
GCCTACTAGAGCAAGAAACCAAGTGTAAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTTACCT  
ACTGTTGTATTGTTATTACAGCTATGCCACTATTAAAGAGCTGTGTAACATCTGGCAAAAAAAA  
AAAAA

## FIGURE 112

MLQDPDSQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVVLKVIDLKYYFLCG  
QPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDN  
FTEALAAETACRQMGYSRAVEIGPDQDLDVVEITENSQELMRNRNSSGPCLSGSLVSLHCLAGKSL  
KTPRVVGGEAASVDSWPWQVSIQYDKQHVCAGSILDPHWVLTAAHCFRKHTDVFNWVKRAGSDKL  
GSFPSLAVAKIIIIIFNPMPYKPDNDIALMKLQFPLTFSGTWRPICLFFFDEELTPATPLWIIGWG  
FTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTQGDGGPLMYQS  
DQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

### Transmembrane domain:

amino acids 32-53 (type II)

### **FIGURE 113**

GGCTGGACTGGAACCTCTGGTCCAAGTGATCCACCCGCCTCAGCCTCCAAAGGTGCTGTGATTA  
TAGGTGTAAGCCACCGTGTCTGCCCTGAACAACCTTTCACTGCAACTAAAAAGCCACAGGAGT  
TGAACTAGCTAGGATTCTGACTATGCTGTGGCTAGTGCTCCTACTCCTACCTACATTAAATC  
TGTTTTTGTTCTCTGTAACTAGCCTTACCTCCTAACACAGAGGATCTGTCACTGTGGCTCT  
GGCCCAAACCTGACCTCACTCTGGAACGAGAACAGAGGTTCTACCCACACCGTCCCCTGAAG  
CCGGGGACAGCCTCACCTGCTGGCCTCTCGCTGGAGCAGTGCCCTACCAACTGTCTACGTCT  
GGAGGCAGTCACTCGGGCAGTGCAAGGTAGCTGAGCCTCTGGTAGCTGCGGCTTCAAGGTGGC  
CTTGCCCTGGCGTAGAAGGGATTTGACAAGCCGAAGATTCATAGGCATGGCTCCACTGCC  
AGGCATCAGCCTGCTGACTCAATCACTGCCCTGGGCCAGGACGGCCGTGGACACCTGCTCA  
GAAGCAGTGGGTGAGACATCACGCTGCCGCCATCTAACCTTTCATGTCCTGCACATCACCTG  
ATCCATGGGCTAATCTGAACTCTGCTCCAAGGAACCCAGAGCTTGAGTGAGCTGTGGCTCAGACC  
CAGAAGGGTCTGCTTAGACCACCTGGTTATGTGACAGGACTTGCAATTCTGGAACATGAGG  
GAACGCCGAGGAAAGCAAAGTGGCAGGGAAAGGAACCTGTGCCAATTATGGTCAGAAAAGATG  
GAGGTGTTGGTTATCACAAGGCATCGAGTCTCTGCATTCACTGGACATGTGGGGAAAGGCTG  
CCGATGGCGCATGACACACTCGGGACTCACCTCTGGGCCATCAGACAGCCGTTCCGCCCGAT  
CCACGTACAGCTGCTGAAGGGCAACTGCAGGCCATGCTCTCATCAGCCAGGCAGCAGCCAAA  
TCTGCATACCAGCCAGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCAATTCTCCCTCC  
CTCCTCCCTCTGAGAGGCCCTCTATGTCCTACTAAAGCCACCAGCAAGACATAGCTGACAGG  
GGCTAATGGCTCAGTGTGGCCAGGAGGTCAAGCAAGGCCAGAGCTGATCAGAAGGCCGTGCT  
GTGCGAACACGGAAATGCCCTCAGTAAGCACAGGCTGCAAATCCCAGGCAAAGGACTGTGTGG  
CTCAATTAAATCATGTTCTAGTAATTGGAGCTGCTTCAAGGAGACTTGATTTGAATTGAAACCCAAATCCA  
CAAATGATCTCCAAGGGCCCTATACCCAGGAGACTTGATTTGAATTGAAACCCAAATCCA  
AACCTAAGAACCAAGGTGCATTAAGAACATCAGTTATTGCCGGGTGTGGTGGCTGTAATGCCAACATGG  
TTGGGAGGCGAGGCAGGTAGATCACCTGAGGTCAAGGAGTTCAAGACCAGGCCAGGCCAACATGG  
TGAAACCCCTGTCTACTAAAAATACAAAAAAACTAGCCAGGCATGGTGGTGTGCTGTATC  
CCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTGAAACCTGGAGGTGAAGGAGGCTGAGACA  
GGAGAACATCACTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAATAAAAAAGAATTA  
TGGTTATTGTAA

## **FIGURE 114**

MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDSLWPKPDLHSGTRTEVSTHTVPSKPGTASPC  
WPLAGAVPSPTVSRLALTRAVQVAEPLGSCGFQGGPCPGRRRD

**Signal peptide:**

amino acids 1-15

## **FIGURE 115**

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGGCAA  
AGAATCCTCCAGAGAATTGTGAAGACTGTACATTCTAAATGCAGAAGCTTTAAATCCAAGAAA  
ATATGTAATCACTTAAGATTGTGGACTGGTGTGTTGGTATCCTGGCCCTAACCTAATTGTCCT  
GTTTGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACATGGAGCACACTT  
TCTACAGCAATGGAGAGAAGAAGATTACATGAAATTGATCCTGTGACCAGAACTGAAATA  
TTCAGAAGCGAAATGGCACTGATGAAACATTGAAAGTGCACGACTTTAAAACGGATACTGG  
CATCTACTCGTGGGTCTCAAAAATGTTTATCAAAACCTCAGATTAAGTGATTCCTGAATT  
CTGAACCAGAAGAGGAAATAGATGAGAATGAAAGAAATTACCAACTTCTTGAAACAGTCAGTG  
ATTGGGTCCCAGCAGAAAGCCTATTGAAAACCGAGATTTCTTAAATCCTGAAACAGTCAGTG  
GATTTGTGATAACGTGACCATGTATTGGATCAATCCCCTCTAATATCAGTTCTGAGTTACAAG  
ACTTTGAGGAGGGAGGAGAAGATCTTCACTTCCCTGCCAACGAAAAAAAGGGATTGAAACAAAT  
GAACAGTGGTGGTCCCTCAAGTGAAGTAGAGAAGACCCGTACGCCAGACAAGCAAGTGAGGA  
AGAACTCCAATAATGACTATACTGAAATGAAATTGATCCCCTGCTGGATGAGAGAG  
GTTATTGTTGATTACTGCCGTCAGGCAACCGCTATTGCCGCCGCTGTGAAACCTTACTA  
GGCTACTACCCATATCCACTGCTACCAAGGAGGACGAGTCATCTGCGTGTCACTGCCCTG  
TAACTGGTGGTGGCCCGCATGCTGGGAGGGCTTAATAGGAGGTTGAGCTCAAATGCTAAAC  
TGCTGGCAACATATAATAATGCTATTCAATGAAATTCTGCCATGAGGCATCTGGCCCT  
GGTAGGCCAGCTCTCCAGAATTACTGTAGGTAATTCTCTCTCATGTTCTAATAAAACTTCTACA  
TTATCACCAAAAAAAAAAAAAAA

## **FIGURE 116**

MAKNPPENCEDCHILNAEAFSKKICKSLKICGLVFGILALTILFWGSKHFWPEVPKKAYDME  
HTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP  
EFSEPEEEIDENEITTTFFEQSVIWVPAEKPIENRDFLKNSKILEICDNVTMYWINPTLISVSE  
LQDFEEEGEDLHFPAKEKKGIEQNEQWVVPQVKVEKTRHARQASEEEELPINDYTENGIEFDPLD  
ERGYCCIYCRRGNRYCRRVCEPLLGYYPYCYQGGRVICRVIMPCNWWVARMLGRV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-40

**Transmembrane domain:**

amino acids 25-47 (type II)

**N-glycosylation sites.**

amino acids 94-97, 180-183

**Glycosaminoglycan attachment sites.**

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

**N-myristoylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 315-317

**Cytochrome c family heme-binding site signature.**

amino acids 9-14

## **FIGURE 117**

GAGCTCCCTCAGGAGCGCGTTAGCTCACACCTCGCAGCAGGGGGCAGCTCTCGCAGGCGCA  
GGCGGGCGGCCAGGATCATGTCCACCACATGCCAAGTGGTGGCGTTCCCTCTGCATCCTGGGCT  
GGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCCAGGACCTGTACGACAACCCCGTCACCT  
CCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTCGTGAGGCAGAGTTCAGGCTTACCGAATGCAGGCC  
TATTCACCATCCTGGACTTCCAGCCATGCTGCAGGCAGTGGAGCCCTGATGATCGTAGGCATCGTCT  
GGGTGCCATTGGCCTCTGGTATCCATCTTGCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTG  
CCAAAGCCAACATGACACTGACCTCCGGATCATGTTCAATTGTCAGGTCTTGTCAGGCAATTGCTGGAGTG  
TCTGTGTTGCCAACATGCTGGTACTAATTCTGGATGTCCACAGCTAACATGTACACCGCAGGGCT  
GATGGTGCAGACTGTTCAAGACCAGGTACACATTGGTGCAGGCTGTTCTGGGCTGGCTGGAGGCC  
TCACACTAATTGGGGGTGTGATGATGTGCATGCCCTGCCGGGCTGGCACCAGAAGAAACCAACTACAAA  
GCCGTTCTTATCATGCCCTCAGGCCACAGTGTGCCTACAAGCCTGGAGGCTCAAGGCCAGCAGTGGCTT  
TGGGTCCAACACCAAAAAACAAGAAGATATACGATGGAGGTGCCGCACAGAGGACGAGGTACAATCTTATC  
CTTCCAAGCAGCAGTATGTGTAATGCTCTAACAGACCTCTCAGCACGGCGGAAGAAACTCCGGAGAGCTCA  
CCCCAAAACAAGGAGATCCCATCTAGATTCTCTGCTTTGACTCACAGCTGAAAGTAGAAAAGCCT  
CGATTTCATCTTGGAGAGGCCAATGGTCTTAGCCTCAGTCTGTCTCAAATATTCCACCATAAAACA  
GCTGAGTTATTATGAATTAGAGGCTATAGCTCACATTTCACATCTCTATTCTTTAAATATAACT  
TTCTACTCTGATGAGAGAATGTGGTTAACATCTCTCACATTGATGATTTAGACAGACTCCCCCTC  
TTCCCTCTAGTCATAAAACCCATTGATGATCTATTCCAGCTTATCCCCAAGAAAATTGGAAAGGAAA  
GAGTAGACCAAAAGATGTTATTCTGCTGTTGAATTGCTCTCCCCACCCCAACTGGCTAGTAATAA  
ACACTTACTGAAGAAGAACAATAAGAGAAAGATATTGTAATCTCTCCAGCCCATGATCTGGTTCTTCTT  
ACACTGTGATCTAAAGTTACCAACCAAAAGTCATTTCAGTTGAGGCAACCAAACCTTCTACTGCTG  
TTGACATCTCTTATTACAGCAACACCATTCTAGGAGTTCTGAGCTCTCCACTGGAGTCTTCTTCT  
CGCGGGTCAGAAAATTGCTCTAGATGAATGAGAAAATTATTTTAAATTAAAGCTTAATATAGTTAA  
AATAAAATAATGTTAGTAAATGATACTATCTCTGAAATAGCTCACCCCTACATGTGGATAGAAG  
GAAATGAAAAATAATTGCTTTGACATTGCTATATGGTACTTTGTAAGTCATGCTTAAGTACAAATTCC  
ATGAAAAGCTCACACCTGTAATCTGACTTTGGAGGCTGAGGAGGAAGGACTACTGAGCCAGAAGT  
TCGAGACTAGCCTGGCAACATGGAGAAGCCCTGCTCTACAAATAACAGAGAGAAAAATGCCAGTC  
TGGTGGCATACACCTGTAATCTGACTTTGGAGGCTGAGGAGGACTACTGAGCCAGGGAGGT  
TGGGGCTGCAGTGAGGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGATCCTGCTAAAAA  
AATAAAAATAATGAAACACAGCAAGTCCTAGGAAGTAGGTTAAAACATAATTCTTTAA

## **FIGURE 118**

MSTTCQVVAFLSILLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLWRSCVRQSSGFTECRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLSIFALKCIRIGSMEDSAKANMTLTSGIMFIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGVWAGGLTLIGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTEDEVQSYP SKHDY  
V

**Signal peptide:**

amino acids 1-23

**Transmembrane domains:**

amino acids 81-100, 121-141, 173-194

## **FIGURE 119**

GGAAAAACTGTTCTCTGTGGCACAGAGAACCTGCTCAAAGCAGAAGTAGCAGTCCGGAGTCC  
AGCTGGCTAAACTCATCCCAGAGGATAATGGCAACCCATGCCTAGAAATCGCTGGCTGTTCTTG  
GTGGTGTGGAATGGGGCACAGTGGCTGTCAGTGCATGCCTCAGTGGAGAGTGTGCGGCCTTCATT  
GAAAACAACATCGTGGTTTGAACACTCTGGGAAGGACTGTGGATGAATTGCGTGAGGCAGGCTAA  
CATCAGGATGCAGTGCAAAATCTATGATCCCTGCTGGCTTTCTCCGGACCTACAGGCAGCCAG  
GACTGATGTGTGCTGCTCCGTGATGTCCTTCTGGCTTCATGATGCCATCCTGGCATGAAATGC  
ACCAGGTGCACGGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTCAT  
CATCACGGGCATGGTGTGCTCATCCCTGTGAGCTGGGTGCCAATGCCATCATCAGAGATTCTATA  
ACTCAATAGTGAATGTTGCCAAAAACGTGAGCTGGAGAAGCTCTACTTAGGATGGACCACGGCA  
CTGGTGCTGATTGTTGGAGGAGCTCTGTTCTGCGTTTGTGCAACGAAAGAGCAGTAGCTA  
CAGATACTCGATAACCTCCCATCGCACAACCCAAAAAGTTATCACACCGGAAAGAAGTCACCGAGCG  
TCTACTCCAGAAGTCAGTATGTTAGTTGTTATGTTTTAACTTACTATAAAGCCATGCAAATG  
ACAAAAATCTATATTACTTCTCAAAATGGACCCCAAAGAAACTTGTGATTACTGTTCTTAACGCCT  
AATCTTAATTACAGGAACGTGCATCAGCTATTATGATTCTATAAGCTATTCAAGCAGAATGAGATA  
TTAAACCAATGCTTGATTGTTAGAAAGTATAGTAATTGTTCTAAGGTGGTCAAGCATTCTA  
CTCTTTTATCATTACTTCAAAATGACATTGCTAAAGACTGCATTATTTACTACTGTAATTCTCC  
ACGACATAGCATTATGTACATAGATGAGTGTAAACATTATCTCACATAGAGACATGCTTATATGGT  
TTTATTAAATGAAATGCCAGTCCATTACACTGAATAAAATAGAAACTCAACTATTGCTTCAGGGAA  
ATCATGGATAGGGTTGAAGAAGGTTACTATTAAATTGTTAAAACAGCTAGGGATTAATGCTCCA  
TTTATAATGAAGATTAAGGCTTAATCAGCATTGTAAGGAAATTGAATGGCTTCTGATAT  
GCTGTTTTAGCCTAGGAGTTAGAAATCCTAACATTCTTATCCTCTCTCCAGAGGCTTTTT  
CTTGTGATTAAATTAAACATTAAACGAGATATTGTCAAGGGCTTGCAATTCAAAGCT  
TTCCAGGGCTACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAGTGTGATGGTTAGGAAAGTG  
AAAATTTTGTGTTGTATTTGAAGAAGAATGATGCAATTGACAAGAAATCATATATGTATGGAT  
ATATTAAATAAGTATTGAGTACAGACTTGAGGTTCATCAATATAAAATAAAAGAGCAGAAAAATA  
TGTCTGGTTTCTTGTACCAAAAAACAAACAAAAAAAGTTGTCTTGTGAGAAACTTCACCT  
GCTCCTATGTGGGTACCTGAGTCAAAATTGTCATTGTTCTGTGAAAATAATTCTTGT  
CCATTCTGTTAGTTACTAAAATGTAAACTGTATTCTGTTATTCAAATTGATGAA  
ACTGACAATCCAATTGAAAGTTGTGTCGACGTCTGCTAGCTAAATGAATGTGTTCTATTGCTT  
TATACATTATTAATAAAATTGTACATTCTAATT

## **FIGURE 120**

MATHALEIAGLFLGGVGMVGTAVTVMPQWRVSIFIENNIVVFENFWEGLWMNCVRQANIRMQCK  
IYDSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILTAGIIFIITG  
MVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTALVLIVGGALFCCVFCCNEKSSY  
RYSIPSHRTTQKSYHTGKKSPSVYRSQYY

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 82-101, 118-145, 164-188

## **FIGURE 121**

GGAGAGAGGCGCGCGGGTGAAAGGCGATTGATGCAGCCTGCGCGGCCTCGGAGCGCGCGAG  
CCAGACCGCTGACCACGTTCTCCTCGGTCTCCTCCGCCTCCAGCTCCCGCTGCCAGCC  
GGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGAGCGGCTCCGCGGCCCTCGCTGCTCC  
TGCTGCTGAGCTGCCCGCCGTGAGCGCCTCTGAGATCCCAAGGGGAAGCAAAGGCGCAG  
CTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCC  
TGGTCGAGACGGGAGCCCTGGGCCAATGTTATTCCGGTACACCTGGATCCCAGGTGGGATG  
GATTCAAAGGAGAAAAGGGGGATGTCTGAGGGAAAGCTTGAGGAGTCTGGACACCCAACTAC  
AAGCAGTGTTCATGGAGTTCAATTGAATTATGGCATAGATCTTGGAAAATTGCGGAGTGTACATT  
TACAAAGATGCGTCAAATAGTGTCTAAGAGTTGTCAGTGGCTCACTTCGGCTAAATGCA  
GAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGTTCAAGGACCTTCCC  
ATTGAAGCTATAATTATTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAAATTATCATCG  
CACTTCTCTGTGGAAGGACTTGTGAAGGAATTGGTGGATTAGTGGATGTTGCTATCTGGG  
TTGGCAGTGTTCAGATTACCCAAAAGGAGATGCTTCACTGGATGGAATTGAGTTCTCGCATC  
ATTATTGAAGAACTACCAAAATAAATGCTTAATTTCATTTGCTACCTTTTTTATTATGCC  
TTGGAATGGTTCACTTAAATGACATTAAATAAGTTATGTATACTCTGAATGAAAAGCAAAG  
CTAAATATGTTACAGACCAAGTGTGATTTCACACTGTTTAAATCTAGCATTTCATTTG  
CTTCAATCAAAAGTGGTTCAATATTTTAGTTGGTTAGAATACTTCTTCAGTCACATT  
CTCTCAACCTATAATTGGAATATTGTTGGTCTTTGTTCTCTTAGTATAGCATTAA  
AAAAAAATAAAAAGCTACCAATCTTGTACAATTGTAAGAATTTTTTATATCTGT  
TAAATAAAAATTATTCCAACA

## **FIGURE 122**

MRPQGPAASPQRRLRGLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGVPGR  
DGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTK  
MRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYYLDQGSPEMNSTINIHRTS  
SVEGLCEGIGAGLVDAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217

## **FIGURE 123**

GCTGAGCGTGTGCGCGTACGGGCTCTCGCTTCTGGCTCCAACGCAGCTGTGGCTGAA  
CTGGGTGCTCATCAGGGAACTGCTGGGCTATGAAATACAGATGTGGCAGCTCAGGTAGCCCCAA  
ATTGCCTGGAAGAATACATCATGTTTGCATAAGAAGAAATTGTAAGGATCCAGTTTTTTTA  
ACCGCCCCCTCCCCACCCCCAAAAAAACTGTAAGAGATGCAAAACGTAATATCCATGAAGATCC  
TATTACCTAGGAAGATTGATTTGCTGCGAATGCCTGTTGGATTATTGTTCTGGAG  
TGGTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCTCCAAGGGTCCAATT  
TCTTCCTGGGTGTCAGCGAGCCTGACTCACTACAGTGACGCTGACAGGGCTGTCATGCAACTG  
GCCCTAAAGCCAAAGCAAAAGACCTAAGGACGACCTTGAACAATACAAGGATGGGTTCAATG  
TAATTAGGCTACTGAGCGGATCAGCTGAGCACTGGTTAGGCCCCACTGTCCTACTGACAATG  
CTTCTCTGCCAACGAGGATGCCCTAAGGGCTGTAGGTGTGAAGGCAAATGGTATTGTA  
ATCTCAGAAATTACAGGAGATAACCTCAAGTATATCTGCTGGTGTAGGTTGTCCTCGCT  
ATAACAGCCTCAAAAACCTAAAGTATAATCAATTAAAGGGCTCAACCAGCTCACCTGGCTATAC  
CTTGACCATAACCATATCAGCAATATTGACGAAAATGCTTTAATGGAATACGCAACTCAAAGA  
GCTGATTCTTAGTCCAATAGAATCTCTATTCTTAACAATACCTTCAGACCTGTGACAATT  
TACGGAACCTGGATCTGCTATACTAGCTGCATTCTGGGATCTGAACAGTTGGGCTTGG  
CGGAAGCTGCTGAGTTACATTACGGCTAACTCCCTGAGAACCATCCCTGTGCGAATATTCCA  
AGACTGCCGCAACCTGGAACTTGGACCTTGGACCTGGGATATAACCGGATCGAAGTTAGCCAGGAATG  
TCTTGCTGGCATGACTCAAGAACATTACCTGGAGCACAATCAATTTCAGCTAAC  
CTGGCCCTTTCCAAGGTTGGTCAGCCTTCAGAACCTTACTTGCAAGTGGAAATAAATCAGTGT  
CATAGGACAGACCATGTCCTGGACCTGGAGCTCCTACAAAGGCTTGATTATCAGGAATGAGA  
TCGAAGCTTCAGTGGACCCAGTGTGTTCCAGTGTGTCCGAATCTGCAAGCCTCAACCTGGAT  
TCCAACAAGCTCACATTATTGGTCAAGAGATTGGATTCTGGATATCCCTCAATGACATCAG  
TCTTGCTGGAAATATGGGAATGCAAGCAGAAATATTGCTCCCTGTAAGGAAACTGGCTGAAAGTT  
TTAAAGGTCAAGGGAGAATACAATTATCTGTCAGTCCCAAAGAGACTGCAAGGAGATAATGTG  
ATCGATGCACTGAAAGAAACTACAGCATCTGTCAGGCAAAGACTCCCTGAGGAGTTGATCTGCCAG  
GGCTCTCCCAAAGCGACGTTAACGCCAAGCTCCCCAGGCCGAAGCATGAGACAACCCCTT  
TGCCCCCGACGGTGGAGCCACAGAGGCCGCCAGAGAACCGATGTCAGGCCGAGCACATCTCT  
TTCCATAAAATCATCGCGGGCAGCGTGGCGTTTCTGTCGTGTCATCCTGCTGGTTAT  
CTACGTGTCATGGAGCGGTACCCCTGCGAGCATGAAGCAGCTGCAAGCAGCAGCTCCCTCATGCGAA  
GGCACAGGAAAAGAAAAGACAGTCCCTAAAGCAAATGACTCCCAAGGAGCACCAGGAATTATGTA  
GATTATAAAACCCACCAACACGGAGACCGAGGAGATGCTGAATGGGACGGGACCCCTGCACCTA  
TAACAAATCGGGCTCCAGGGAGTGTGAGGTATGAACTGTGATAAAAAGAGCTTAAAGCT  
GGGAAATAAGTGGTGTATTGAACTCTGGTACTATCAAGGGAAACGCGATGCCCTCCCTCC  
TTCCCTCTCCCTCACTTGGTGGCAAGATCCTTCCTGTCGTTAGTGCATTCAATACT  
GGTCATTTCTCTCATACATATCAACCCATTGAAATTAAATACCAACAATCAATGTGAAGCTT  
GAACCTCGGTTAAATAATACCTATTGTATAAGACCTTACTGATTCCATTAAATGTCGCAATT  
GTTTAAGATAAAACTCTTCATAGTAAAAAA

## **FIGURE 124**

MGFNVIRLLSGSAVALVIAPTVLLTMLSSAERGCPKGCRCEGKMVYCESQKLQEIPSSISAGCLG  
LSLRYNSQLQKLKYNQFKGLNQLTWLYLDHNHISNIDENAFNGIRRLKELILSSNRISYFLNNTR  
PVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHRSNSLRTIPVRIQDCRNLELLDLGYNRIRS  
LARNVFAGMIRLKELHLEHNQFSKLNLAFLPRLVSLQNLQWNKISVIGQTMSTWSSLQRLDL  
SGNEIEAFSGPSVFQCVPNLQRLNLDNSNKLFIGQEILDWSWISLNDISLAGNIWECSRNICSLVN  
WLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLARALPKPTFKPKLPRKHE  
SKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVLIVYVSWKRYPASMKQLOQR  
SLMRRHRKKRQSLKQMTPSTQEFYVDYKPTNTETSEMLLNGTGPCTYNKSGSRECEV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 420-442

**N-glycosylation sites.**

amino acids 126-129, 357-360, 496-499, 504-507

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 465-468

**Tyrosine kinase phosphorylation site.**

amino acids 136-142

**N-myristylation sites.**

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

## **FIGURE 125**

CCGTTATCGTCTTGCCTACTGCTGAATGTCGTCGGAGGAGGAGGCTTGTCCGCTG  
ACCCAGAGATGGCCCGAGCGAGCAAATTCCACTGTCCGGCTGCGCGCTACCGTGGCGAGCT  
AGCAACCTTCCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAGCTTGCTC  
GGTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCACAGCCCTAGGGATC  
ATTGAAGAGGAAGGTTCTAAAGCTTGGCAAGGAGTGACACCCGCCATTACAGACACGTAGT  
GTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTGTGTTGGCAAAGTGAAG  
ATGAGCATTATCCCCTTGGAAATCAGTCATTGGAGGGATGATGGCTGGTGTATTGGCAGTT  
TTAGCCAATCCAACTGACCTAGTGAAGGTTCAGATGCAATGGAAGGAAAAGGAACTGGAAGG  
AAAACCATTGCGATTCGTGGTACATCATGCATTGCAAAATCTTAGCTGAAGGAGGAATAC  
GAGGGCTTGGCAGGCTGGTACCAATATAAAAGAGCAGCACTGGTAATATGGGAGATTA  
ACCACTTATGATAACTGAAACACTACTTGGTATTGAATACACCACTTGAGGACAATATCATGAC  
TCACGGTTATCAAGTTATGTTCTGGACTGGTAGCTCTATTCTGGAACACCAGCGATGTCA  
TCAAAAGCAGAATAATGAATCAACCACGAGATAAAACAAGGAAGGGACTTTGTATAATCATCG  
ACTGACTGCTTGATTCAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAAGGCTTTTAC  
ATCTTGGCTGAGAATGACCCCTGGTCAATGGTGTCTGGCTACTTATGAAAAATCAGAGAGA  
TGAGTGGAGTCAGTCCATTTTAA

## **FIGURE 126**

MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMQGEAALARLGDGARES  
APYRGMVRTALGIIEEGFLKLWQGVTPAIYRHVVYSGGRMVTYEHLREVVFGKSEDEHYPLWKS  
VIGGMMAGVIGQFLANPTDLVKVQMOMEGKRKLEGKPLRFRGVHAFAKILAEGGIRGLWAGWVP  
NIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSDLVASILGTPADVIKSrimnQP  
RDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTPWSMVFWLTYEKIREMSGVSPF

**Transmembrane domains:**

amino acids 25-38, 130-147, 233-248

## FIGURE 127

CGCGGATCGGACCAAGCAGGTGGCGCGCGCAGGAGAGCGGCCGGCGTCAGCTCCTCGAC  
CCCCGTGTCGGGCTAGTCCAGCGAGGCGGACGGCGGCGTGGGCCATGGCCAGGCCGGCATGG  
AGCGGTGGCGCGACCGCTGGCGCTGGTACGGGGCCTCGGGGGCATCGGCAGGCCGTGGCC  
CGGGCCCTGGTCCAGCAGGGACTGAAGGTGGTGGCTGCGCCCGACTGTGGCAACATCGAGGA  
GCTGGCTGCTGAATGTAAGAGTCAGGCTACCCCAGGACTTGTACAGATGTGACCTAT  
CAAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGCGGTGAGACATC  
TGCATCAACAATGCTGGCTTGGCCCGGCCTGACACCCCTGCTCTCAGGCAGCACCAAGTGGTTGGAA  
GGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACACGGGAAGCCTACCAAGTCCATGA  
AGGAGCGGAATGTGGACGATGGCACATCATTAACATCAATAGCATGCTGGCCACCGAGTGTAA  
CCCCTGTCGTGACCCACTTCTATAGGCCACCAAGTATGCCGTACTGCCGTGACAGAGGGACT  
GAGGCAAGAGCTCGGGAGGCCAGACCCACATCCGAGGCCACGTGCATCTCCAGGTGTGGTGG  
AGACACAATTGCCCTCAAACCTCACGACAAGGACCTGAGAAGGCAGTGCACCTATGAGCAA  
ATGAAGTGTCTCAAACCGAGGATGTGGCCAGGGCTGTATCTACGCTCAGCACCCCCGACA  
CATCCAGATTGGAGACATCCAGATGAGGCCACGGAGCAGGTGACACTGTGGAGCTCC  
TCCTTCCCTCCCCACCCCTCATGGCTTGCCCTGCCTCTGGATTAGGTGTTGATTCGGAT  
CACGGGATACCACTCCTGTCCACACCCCGACCAGGGCTAGAAAATTGTTGAGATTTTATA  
TCATTTGTCAAATTGCTTCAGTTGTAATGTGAAAATGGCTGGGAAAGGAGGTGGTGTCCC  
TAATTGTTTACTTGTAACTTGTCTTGCCCTGGGACTTGGCTTGTGCTCTCAGTG  
TCTTCCCTTGACATGGAAAGGAGTTGTGGCCAAATCCCCATCTTGCACCTCAACGTCTG  
TGGCTCAGGGCTGGGTGGCAGAGGGAGGCCACCTTACCTTATCTGTGTTGTTATCCAGGGCTCC  
AGACTTCCCTCTGCCCTGCCCCACTGCACCCCTCTCCCCCTATCTATCTCCTCTCGGCTCCCC  
AGCCCAGTCTGGCTTGTCCCCCTGGGGTACCCCTCACTCTGACTCTGACTATGGCAG  
CAGAACACCAGGGCTGGCCAGTGGATTTCATGGTGATCATTAAAAAGAAAAATCGCAACCAA  
AAAAAA

## **FIGURE 128**

MARPGMERWRDRLALVTGASGGIGAAVARALVQQGLKVVGCARTVGNIEELAAECKSAGYPGTLI  
PYRCDLNEEDILSMFSAIRSQHSGVDICINNAGLARPDTLLSGSTSGWKDMFNVNVLALSICTR  
EAYQSMKERNVDDGHIININMSGHRLPLSVTHFYSATKYAVTALTEGLRQELREAQTHIRATC  
ISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**N-myristoylation sites.**

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,  
199-205

**Short-chain alcohol dehydrogenase.**

amino acids 30-42, 104-114

## **FIGURE 129**

AACTTCTACATGGGCCTCCTGCTGGTGCCTTCCTCAGCCTCCTGCCGGTGCCTACACCAT  
CATGTCCCTCCACCCCTCTTGACTGCAGGCGTCAGGTGCAGAGTCAGTCAGTTGCCCGGGAGC  
ACCTCCCCCTCCGAGGCAGTCTGCTCAGAGGGCCTGGCCAGAATTCCAGTTCTGGTTTCATGC  
CAGCCTGTAAGGGCATGGAACTTGGGTGAATCACCGATGCCATTAAAGAGGGTTCTGCCA  
GGATGGAAATGTTAGGTCGTTCTGTGCTGCGCTGTTCATTTAGCAGTAGCCACCAGCCACCTGTGG  
CCGTTGAGTGCTTGAAAATGAGGAACTGAGAAAATTAAATTCTCATGTATTTCATTTATTAA  
TTAATTTTAACTGATAGTTGACATATTGGGGTACATGTGATATTGGATACATGTATAACAA  
TATATAATGATCAAATCAGGGTACTGGATATCCATCACATCAAACATTATTTTATTCTT  
TTAGACAGAGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTGGTGCCATCTCAGCTTACTGCAAC  
CTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCTCCACCTCCAAGTAGCTGGACTACAGGCAT  
GCACCACAATGCCCAACTAATTGGTATTAGTAGAGACGGGGTTTGCCATGTTGCCAGG  
CTGGCCTTGAACTCCTGGCCTCAAACAAATCCACTGCCTCGGCCTCCAAAGTGTATGATTACA  
GGCGTGAGCCACCGTGCCTGGCTAAACATTTATCTTCTTGTTGGAACTTGAAATTAT  
ACAATGAATTATTGTTAACTGTCATCTCCCTGCTGTGCTATGGAACACTGGGACTTCTTCCCTCT  
ATCTAACTGTATATTGTACCAGTACTTACCAACCGTACTTCATCCCCACTCCTCTATCCTTCCC  
AACCTGTGATCACCTCATTCTACTCTACCTCCATGAGATCCACTTTTAGCTCCCACATGTG  
AGTAAGAAAATGCAATATTGTCTTCTGTGCTGGCTTATTCATTAACATAATGACTTCTG  
TTCCATCCATGTTGCTGCAAAATGACAGGATTCGTTCTTAATTCATTAACATAACCACACATG  
GCAAAAAA

## **FIGURE 130**

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFRCRVSVAREHLPSPRGSSLRGPRPRIPVLVSCQPV  
KGHGTLGESPMMPFKRVFCQDGTVRSFCVCAVFSSHQPPVAVECLK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-18

**N-myristoylation site.**

amino acids 86-92

**Zinc carboxypeptidases, zinc-binding region 2 signature.**

amino acids 68-79

## **FIGURE 131**

TTCTGAAGTAACGGAAGCTACCTTGATAAAGACCTAACACTGCTGACCATGATCAGCGCAGCCTGGAGC  
ATCTTCCTCATCGGGACTAAAATTGGGCTGTCCTCAAGTAGCACCTCTATCACTTATGGCTAAATCTG  
TCCATCTGTGTGTCGCTGCGATGCGGGTTTCATTACTGTAATGATCGCTTCTGACATCCATTCAAACAG  
GAATACCAGAGGATGCTACAACTCTACCTCAGAACAAACAAATAATGCTGGATTCTTCAGAT  
TTGAAAAACTTGCTGAAAGTAGAAAGAATATACTATACCAACAGTTAGATGAATTCTACCAACCT  
CCCAAAGTATGAAAGAGTTACATTTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTCAA  
AAATTCCCTATCTGGAAGAATTACATTAGATGACAACCTGTCCTGAGTTAGCATAGAAGAGGGAGCA  
TTCCGAGACAGCAACTATCTCGACTGCTTTCTGTCGGTAATCACCTAGCACAATTCCCTGGGTT  
GCCAGGACTATAGAAGAACTACGCTGGATGATAATCGCATATCCACTATTCATCACCATCTCTCAAG  
GTCTCACTAGTCTAAACGCTGGTCTAGATGAAACCTGTTGAACAATCATGGTTAGGTGACAAGTT  
TTCTTCACCTAGTTAATTGACAGAGCTGTCCTGGTGCAGAATTCCCTGACTGCTGACCAAGTAAACCT  
TCCAGGCACAAACCTGAGGAAGCTTATCTCAAGATAACCACATCAATCGGGTGCCTTAAATGCTTTT  
CTTATCTAAGGCAGCTATCGACTGGATATGCCAATAAACCTAAGTAATTACCTCAGGGTATCTT  
GATGATTGGACAATATAACACAACGATTCTCGAACAAATCCCTGTTGCGGGTCAAGATGAAATG  
GGTACGTAACGGTACAATCACTACCTGTGAAGGTCAACGTGCGTGGGCTCATGTGCCAACCCCCAGAAA  
AGGTTGGTGGATGGCTATTAAGGATCTCAATGCAAGACTGTTGATTGTAAGGACAGTGGGATTGTAAGC  
ACCATTCAAGATAACCACGCAATACCCAAACACACTGATCTGCCAACGGACAGTGGCCAGCTCAGTGAC  
CAAACAGCCAGATATTAAGAACCCAAAGCTCACTAAGGATCAACAAACCAAGGGAGTCCCTCAAGAAAAAA  
CAATTACAATTACTGTGAAGTCTGCACCTGTACATACCATTCAATCTCTGGAAACTGCTCTACCTATG  
ACTGTTGAGACTCAGCTGGTTAAACTGGCCATAGCCCGCATGGATCTATAACAGAAACAATTGT  
AACAGGGAAACGCAGTGAGTACTGGTCACAGCCCTGGAGCCTGATTCCCTATAAGATGATGGTTC  
CCATGGAAACAGCAACCTCTACCTTGTGAAACTCCTGTTGATTGAGACTGAAACTGCACCCCTT  
CGAATGTACAACCTACAACCAACCCCTCAATCGAGACCAAGAGAAAGAACCTTACAAAACCCAAATTAC  
TTGGCTGCCATCTGGTGGGGCTGTCGGCCCTGGTTACCATGGCTTCTGCTTGTGTTGGTATG  
TTCATAGGAATGGATCGCTTCTCAAGGAACGTGCAATAGCAAAGGGAGGAGAAGAAAGGATGACTAT  
GCAGAACGCTGGCACTAAGAAGGACAACCTATCCCTGAAATCAGGGAAACTCTTCAAGATGTTACCAAT  
AAGCAATGAACCCATCTGAAGGAGGAGTTGTAATACACCCATATTCTCTCAATGGAATGAATCTGT  
ACAAAAACAAATCACAGTGAAGCAGTAGTAACCGAAGCTACAGAGACAGTGGTATTCCAGACTCAGATCAC  
TCACACTCATGATGCTGAAGGACTCACAGCAGACTTGTGTTGGTTTTAACCTAAGGGAGGTGATG  
GT

## **FIGURE 132**

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRC DAGFIYCNDRFLTSIPTGIPEDATTLYL  
QNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKE LHQENNIRTITYDSSL SKI PYL  
EELHLDNSVSAVSIEEGAFRDSNYLRLLFLSRNHLS TIPWGLPRTIEELRLDDNRISTISSPSL  
QGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTE SLVRNSLTAAPVNLPGTNLRKLYLQDNHIN  
RVPPNAFSYLRQLYR LDMSNNNLSNLPQGIFDDLDNITQLI LRNNPWC GCKMKWV RDWLQSLPV  
KVNVRGILMCQAPEKVRGMAIKDLNAELFDCKDSGIVSTI QTIA PNTVPAQGQWPAPVTKQPD  
IKNPKLTKDQQTTGSPSRKTITITVKS VTS DTIHISWKLALPMTALRLS WLKLGHSPAFGSITET  
IVTGERSEYLVTALEPDSPYKCMVPMETSNLYLFDETPVCIETETAPLRMYNPTTLNREQEKE  
PYKNPNLPLAAIIGGAVALVTIALLALVCWYVHRNGSLFSRNCAYSKGRRKDDYAEAGTKKD NS  
ILEIRETSFQMLPISNEPISKEE FVIHTIFPPNGMNLYKNNHSESSSNRSYRDSGIPDSDHSHS

**Important features of the protein:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 531-552

**N-glycosylation sites.**

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

**Tyrosine kinase phosphorylation site.**

amino acids 515-522

**N-myristoylation sites.**

amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,

640-645

**Amidation site.**

amino acids 567-570

**Leucine zipper pattern.**

amino acids 159-180

**Phospholipase A2 aspartic acid active site.**

amino acids 34-44

### **FIGURE 1.33**

CCGTCACTCCCCCTGCAGCCACCCCTCCCAGAGTCCTTGCCCAGGCCACCCAGGCTTCTGGCA  
GCCCTGCCGGGCCACTTGTCTTCCATGTCTGCCAGGGGAGGTGGAAAGGAGGTGGAGGAGGGCG  
TGCAGAGGCAGTCTGGGCTTGGCCAGAGCTCAGGGTGCTGAGCGTGTGACCAGCAGTGAGCAGAG  
GCCGGCCATGGCCAGCCTGGGCTGCTGCTCTGCTTACTGACAGCACTGCCACCGCTGTGGT  
CCTCCTCACTGCCTGGGCTGGACACTGCTGAAAGTAAAGCCACCATTGCAGACACTGATCCTGTCT  
GCGCTGGAGAGAGCACCAGCTTCCTAGAACAGAGGCTGCCTGAAATCAACCTGGATGGCATGGT  
GGGGGTCCAGTGCTGGAAGAGCAGCTAAAAGTGTCCGGAGAAGTGGGCCAGGAGCCCTGC  
TGCAGCCGCTGAGCCTGCGCGTGGGATGCTGGGGAGAAGCTGGAGGCTGCCATCCAGAGATCC  
CTCCACTACCTCAAGCTGAGTGATCCAAAGTACCTAACAGAGAGTCCAGCTGACCCCTCAGCCGG  
GTTTGAAAGCTCCCACATGCCCTGGATCCACACTGATGCCCTTGGTGTACCCACGTTGGC  
CCCAGGACTCATTCTCAGAGGAGAGAAGTGACGTGCGCTGGTGCAGCTGCTGGAACCGGGACG  
GACAGCAGCGAGCCCTGCGGCCCTCAGACCTCTGCAGGAGCCTCATGACCAAGCCGGCTGCTC  
AGGCTACTGCCCTGTCACCAACTGCTCTTCCCTGGGAGAATGAGGGATGCACACAGG  
GACCACCTCAACAGAGCCAGGACTATATCAACCTCTGCGCCACATGATGGACTTGAAACCG  
AGAGCTGAGGCCATGGATACGCCAACCTACCCGGACATCTTCATGGAAAACATCATGTTCTG  
TGGAAATGGGGGGCTCTCCGACTTCTACAAGCTCCGGTGGCTGGAGGCCATTCTCAGCTGGCAGA  
AACAGCAGGAAGGATGCTCGGGGAGCCTGATGCTGAAGATGAAGAATTATCTAAAGCTATTCAA  
TATCAGCAGCATTTCGAGGGAGGTGAAGAGGCGAGAAAAAACATTCCAGATTCTCGCTCTGT  
TGCTCAGGCTGGAGTACAGTGGCGCAATCTGGCTCACTGCAACCTTGCCCTGGTTCAAGC  
AATTCTTCTGCCATCCTCCGAGTAGCTGGACTACAGGAGCGTGCACCATCTGGCTAAT  
TTTATATTTTTAGAGACAGGGTTCATCATGTTGCTCATGCTGGTCTCGAACCTCTGAT  
CTCAAGAGATCCGCCACCTCAGGCTCCAAAGTGTGGATTTAAGGTGTGAGCCACCGTGTCTG  
GCTGAAAAGCACTTCAAAGAGACTGTGTTGAATAAAGGGCCAAGGTTCTGCCACCCAGCACTC  
ATGGGGCTCTCCCTAGATGGCTGCTCCCTCCAAACACAGCCACAGCAGTGGCAGCCCTGG  
GTGGCTTCTATACATCCTGGCAGAATACCCCCCAGCAAACAGAGGCCACACCCATCCACACCG  
CCACCAAGCAGCGCTGAGACGGACGGTCCATGCCAGCTGCCCTGGAGGAGGAACAGACCC  
TTAGTCCTCATCCCTAGATCCTGGAGGGCACGGATCACATCCTGGGAAGAAGGCATCTGGAGG  
ATAAGCAAAGCCACCCGACACCAATCTGGAAGCCCTGAGTAGGCAGGGCCAGGGTAGGTGGG  
GGCCGGGAGGGACCCAGGTGTGAACGGATAAAAGTCAACTGCAACTGAAACTGAAAAAAA

## **FIGURE 134**

MSARGRWEGGGRRACRGSGLARAQGAERVTSSEQRPMASLGLLLLLTLAPPLWSSSLPGLD  
TAESKATIADLILSALERATVFQRLPEINLDGMGVVRVLEEQLKSVREKWAQEPLLQPLSLRV  
GMLGEKLEAAIQRSLHYLKLSDPKYLREFQLTLQPGFWKLPHAWIHTDASLVYPTFGPQDSFSEE  
RSDVCLVQLLGTGTDSEPCGLSDLCRSLMTKPGCSGYCLSHQLLFFLWARMRGCTQGPLQQSQD  
YINLFCANMMDLNRRAEAIGYAYPTRDIFMENIMFCGMGGFSDFYKLRWLEAISWQKQQEGCFG  
EPDAEDEELSKAIQYQQHFSRRVKRREKQFPDSRSVAQAGVQWRNLGSLQPLPPGFQFSCLILP  
SSWDYRSVPPYLANFYIFLVETGFHHVAHAGLELLISRDPPTSGSQSVGL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 39-56

**Tyrosine kinase phosphorylation sites.**

amino acids 149-156, 274-282

**N-myristoylation sites.**

amino acids 10-16, 20-26, 63-69, 208-214

**Amidation site.**

amino acids 10-14

**Glycoprotein hormones beta chain signature 1.**

amino acids 230-237

### **FIGURE 135**

GGTCTGAGTGCAGAGCTGCTGTCATGGCGGCCGCTCTGTGGGCTTCTTCCGTCCTGCTGCTG  
CTGCTGCTATCGGGGATGTCCAGAGCTGGAGGTGCCGGGCTGCTGCTGAGGGATCGGAGG  
GAGTGGGTGGCATAGGAGATCGCTCAAGATTGAGGGCGTAGCTGGTAGACGGAGAAGAGCACGTCGGTTCTTAAG  
CTCAGGACTGGATCTCGCGGCCGAGTGTGGTAGACGGAGAAGAGCACGTCGGTTCTTAAG  
ACAGATGGAGTTGTGGTTCATGATATACTCTGGATCTTATGTAGTGGAAAGTTGTATCTCC  
AGCTTACAGATTTGATCCCGTTGAGTGGATATCACTTCGAAAGGAAAATGAGAGCAAGATAG  
TGAATTACATAAAACATCAGAGGTTGTCAAGACTGCCCTATCCTCTCCAAATGAAATCTCAGGT  
CCACCTTCTTACTTTATTAAAAGGAATCGTGGGCTGGACAGACTTCTAATGAACCCAATGGT  
TATGATGATGGTCTTCCTTATTGATATTGTGCTCTGCCTAAAGTGGTCAACACAAGTGATC  
CTGACATGAGACGGAAATGGAGCAGTCATGAATATGCTGAATTCCAACCATGAGTTGCCTGAT  
GTTTCTGAGTTCATGACAAGACTCTCTCTCAAAATCATCTGGCAAATCTAGCAGCGGCAGCAG  
TAAAACAGGCAAAAGTGGGCTGGCAAAAGGAGGTAGTCAGGCCGTCCAGAGCTGGCATTGCAC  
AAACACGGCAACACTGGGTGGCATCCAAGTCTGGAAAACCGTGTGAAGCAACTACTATAAAACTT  
GAGTCATCCCGACGTTGATCTTACAACGTGTATGTT  
AACTTTTAGCACATGTTGTACTTGGTACACGAGAAAACCCAGCTTCATCTTGCTGTAT  
GAGGTCAATATTGATGTCACTGAATTAATTACAGTGTCTATAGAAAATGCCATTAATAAAATTAT  
ATGAACACTACATTATGTATTAATTAAAACATCTTAATCCAGAAATCAAAAAAAAAAAAA  
AAAAAAAAAAAAAAA

## **FIGURE 136**

MAAALWGFFPVLLLLLSDVQSSEVPGAAEGSGSGVGIGDRFKIEGRAVPGVKPQDWISAA  
RVLVDGEEHVGFLLKTDGSFVVHDIPSGSYVVEVVS PAYRFDPVRVDITSKGKMRARYVNYIKTSE  
VVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMVLPLLIFVLLPKVVNTSDPDMRREME  
QSMNMLNSNHELPDVSEFMTRLFSSKGSSGSSKTGKSGAGKRR

**Important features of the protein:**

**Signal sequence:**

amino acids 1-23

**Transmembrane domain:**

amino acids 161-182

**N-glycosylation site.**

amino acids 184-187

**Glycosaminoglycan attachment sites.**

amino acids 37-40, 236-239

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 151-154

**N-myristoylation sites.**

amino acids 33-38, 36-41, 38-44, 229-234

**Amidation site.**

amino acids 238-241

**ATP/GTP-binding site motif A (P-loop).**

amino acids 229-236

## **FIGURE 137**

GATGGCGCAGCCACAGCTCTGTGAGATTGATTCGATTCTCCCCAGTTCCCTGTGGGTCTGAGGGGA  
CCAGAAGGGTGAGCTACGTTGGCTTCTGAAAGGGGAGGCTATATGCGTCAATTCCCCAAACAA  
GTTTGACATTCCCCCTGAAATGTCATTCTATCTATTCACTGCAAGTGCCTGCTGTTCCAGGC  
CTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGACAGAATAAGGAGCCACGACCTGTGC  
CACCAACTCGCACTCAGACTCTGAACCTCAGACCTGAAATCTTCTTCACGGGAGGCTTGGCAGT  
TTTCTTACTCCTGTGGCTCCAGATTCAGGCCTAAGATGAAAGCCTCTAGTCTGCCTTCAGC  
CTTCTCTGCTGCGTTTATCTCTATGGACTCCTCCACTGGACTGAAGACACTCAATTGGG  
AAGCTGTGTGATGCCACAAACCTCAGGAAATACGAAATGGATTTCTGAGATAACGGGCAGTG  
TGCAAGCCAAGATGAAACATTGACATCAGAATCTAAGGAGGACTGAGTCTTGCAAGACACA  
AAGCCTGCGAATCGATGCTGCCCTGCGCCATTGCTAAGACTCTATCTGGACAGGGTATTAA  
AAACTACCAGACCCCTGACCATTATACTCTCCGAAGATCAGCAGCCTCGCCAATTCTTTCTA  
CCATCAAGAAGGACCTCCGGCTCTCATGCCACATGACATGCCATTGTGGGAGGAAGCAATG  
AAGAAATACAGCCAGATTGAGTCACTTGAAAAGCTGAAACCTCAGGCAGCAGTTGTGAAGGC  
TTTGGGGAACTAGACATTCTCTGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGTGCTG  
CTGCTAAGAATATTGAGGTCAAGAGCTCCAGTCTCAATACCTGCAAGAGGAGGATGACCCAA  
ACCACCATCTTTACTGTACTAGTCTGTGCTGGTCACAGTGTATCTTATTGCTTGCATTACTTG  
CTTCCTTGCAATGATTGTCTTATGCATCCCCAATCTTAATTGAGACCATACTTGCTATAAGATT  
TGTAATATCTTCTGCTATTGGATATATTATTAGTTAATATATTATTATTGCTATT  
ATGTATTTATTTTTACTGGACATGAAACTTAAAAAAATTACAGATTATTTATAACCTG  
ACTAGAGCAGGTGATGTATTTTATACAGTAAAAAAACCTTGTAAATTCTAGAAGAGTGG  
CTAGGGGGTTATTCATTGCTTCAACTAAGGACATATTACTCATGCTGATGCTCTGTGAGAT  
ATTGAAATTGAACCAATGACTACTTAGGATGGGTTGGAATAAGTTTGATGTGAAATTGCAC  
ATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATATTGTGTATCTCCAG  
CCAGGAATCCTACACGGCCAGCATGTATTCTACAAATAAGTTCTTGCATACCAAAAAAAA  
AAAAAAAAAAA

## **FIGURE 138**

MRQFPKTSFDISPEMSFSIYSLQVPAVGLTCWALTAEPGWGQNKGATTCATNSHSDSELRPEIF  
SSREAWQFFLLLWSPDFRPKMASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNG  
FSEIRGSVQAKDGNIDIRILRRTESLQDTK PANRCCLRHLLRLYLDdrvFKNYQTPDHYTLRKIS  
SLANSFLTIKKDLRLSHAHMTCHC GEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEET  
E

**Important features of the protein:**

**Signal peptide:**

amino acids 1-42

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 192-195, 225-228

**N-myristoylation sites.**

amino acids 42-47, 46-51, 136-141

## **FIGURE 139**

CCTGGAGCCGGAAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTCGGTTCGCATCCAGCC  
TAGCGTGTCCACCGATGCCGCTGGGCTCCGGGACTTCGCTACCTGTCGTAGCGATCGAGGTGC  
TAGGGATCGCGGTCTTCCTCGGGATTCTCCCGGCTCCCGTCTGCTCCCTGCCAGAGCGAA  
CACGGAGCGGAGCCCCCAGCGCCCGAACCCCTCGGCTGGAGCCAGTTCAACTGGACCACGCTGCC  
ACCACCTCTTCAGTAAAGTTGTTATTGTCGTAGATAGATGCCCTGAGAGATGATTTGTTG  
GGTCAAAGGGTGTGAAATTATGCCCTACACAACCTACCTGTTGGAAAAGGAGCATCTCACAGT  
TTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCCTGAATCAAGGCATTGATGACGGGGAG  
CCTTCCTGGCTTGTGACGTCACTAGGAACCTCAATTCTCCTGCACTGCTGGAAAGACAGTGTGA  
TAAGACAAGCAAAGCAGCTGGAAAAGAATAGTCTTTATGGAGATGAAACCTGGTTAAATTA  
TTCCCAAAGCATTGTGGAATATGATGGAACACCTCATTTCGTCAGATTACACAGAGGT  
GGATAATAATGTACGAGGCATTGGATAAAGTATTAAAAAGAGGGAGATTGGACATATTAATCC  
TCCACTACCTGGGGTGGACCAATTGGCACATTTCAGGGCCAACAGCCCCCTGATTGGCAG  
AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGCACTGCAAGGGAGAGAGA  
GACGCCCTTACCCATTGCTGGTTCTTGTCGACATGGCATGTCGTGAAACAGGAAGTCACG  
GGGCCTCCTCCACCGAGGGAGGTGAATACACCTCTGATTAACTCAGTTCTGCGTTGAAAGGAAA  
CCCGGTGATATCCGACATCCAAGCACGTCCAATAGACGGATGTGGCTGCGACACTGGCAGTAGC  
ACTTGGCTTACCGATTCCAAAAGACAGTGTAGGGAGCCTCTATTCCAGTTGTGGAAGGAAGAC  
CAATGAGAGAGCAGTTGAGATTTCATTTGAATACAGTGCAGCTAGTAAACTGTTGCAAGAG  
AATGTGCCGTATGAAAAAGATCCTGGGTTGAGCAGTTAAATGTCAGAAAGATTGCAATTG  
GAACCTGGATCAGACTGTACTTGGAGGAAAAGCATTCAAGAGTCTATTCAACCTGGCTCCAAGG  
TTCTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAGTGGCCAG  
TTCTCACCCCTGCTCTGCTCAGCGTCCCACAGGCACTGCACTGACAGAAAGGCTGAGCTGGAAGTCCA  
CTGTCATCTCCTGGTTTCTGCTCTTATTGGTATCCTGTTCTTCCGGCCGTTACGT  
CATTGGTGTGCACCTCAGCTGAAAGTTCGTCGACTTCTGTCGCTACTCTGTCGCTGCTGGCAGGCT  
GCCTTCGTTACCAAGACTCTGGTTGAACACCTGGTGTGCCAAGTGTGGCAGTGCACACTGGAC  
AGGGGGCCTCAGGGAAAGGACGTGGAGCAGCCTTATCCCAGGCTCTGGGTGTCCCACACAGGTG  
TTCACATCTGTCGTCAGGTCAAGTGCCTAGTTCTGAAAGCTAGGTTCTGCGACTGTTAC  
CAAGGTGATTGTAAGAGCTGGCGTCACAGAGAACAGCCCCCAGCTGAGGGGTGTGTGAA  
TCGGACAGCCTCCACAGAGGTGTGGGAGCTGCACTGAGGGAAAGAAGACAAATCGGCCTGGA  
CACTCAGGGAGGTCAAAAGGAGACTTGGTCGACACTCATCCTGCCACCCCCAGAACATGCATCCT  
GCCTCATCAGGTCCAGATTCTTCAAGGGGACGTTTCTGTTGAAATTCTTAGTCCTGGCC  
TCGGACACCTCATCGTTAGCTGGGGAGTGGTGGTGAAGCAGTGAAGAAGAGCGGATGGTCAC  
ACTCAGATCCACAGAGCCCAGGATCAAGGGACCCACTGCACTGAGGCACTGTTGGCCCC  
ACCCCAACCCCTGCACAGCCCTATCCCCTTGGCTTGAGCGTCAGAGGCCCTGTGCTGAGTGT  
CTGACCGAGACACTCACAGCTTGTCACTCAGGGCACAGGCTCTCGAGGCCAGGATGATCTGTG  
CCACGCTTGCACCTCGGGCCATCTGGCTCATGCTCTCTGCTATTGAATTAGTACCTAG  
CTGCACACAGTATGAGTTACCAAAAGAATAAACGGCAATAATTGAGAAAAAAA

## **FIGURE 140**

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPPEPSAGASSNWTLPPPLF  
SKVVIVILIDALRDDVFGSKGVKFMPYTTYLVEKGASHSFVAEAKPPTVTMPRIKALMTGSLPGF  
VDVIRNLNSPALLEDSVIROAKAAGKRIVFYGDETWVKLFPKHFVEYDGTTSFVSDYTEVDNNV  
TRHLDKVLKRGDWDILILHYLGLDHIGHISGPNSPLIGQKLSEMDSVLMKIHTSLQSKERETPLP  
NLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-34

**Transmembrane domain:**

amino acids 58-76

**N-glycosylation sites.**

amino acids 56-60, 194-198

**N-myristylation sites.**

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,  
275-281, 278-284

**Amidation site.**

amino acids 154-158

**Cell attachment sequence.**

amino acids 205-208

## FIGURE 141

GGCACGAGGCAAGCCTTCCAGGGTATCGTGACGCACCTTGAAAGTCTGAGAGCTACTGCCCTACAGAAAGTTACTAGTGCCTAAAGCTGGCGCTGGCACTGATTGTTACTGCTGCTGTTGGAGTACAACTTCCCTATAGAAAACAACTGCCAGCACCTTAAGACCACTCACACCTTCAGAGTGAAGAAACTTAAACCCGAAGAAATTCGCATTCATGACCAGGATCACAAAGTACTGGCCTGGACTCTGGGAATCTCATAGCAGTTCAGATAAAAACTACATACGCCAGAGATCTTCTTGCATTAGCCTCATCCTTGAGCTCAGCCTCTGCGGAGAAAGGAAGTCCGATTCTCCTGGGGTCTCTAAAGGGGAGTTTGTCTACTGTGACAAGGATAAAGGACAAAGTCATCCATCCCTTCAGCTGAAGAAGGAGAAACTGATGAAGCTGGCTGCCAAAAGGAATCAGCACGCCGCCCTCATCTTATAGGGCTCAGGGGGCTCCTGGAAACATGCTGGAGTCGGCGCTACCCCGGATGGTCATCTGCACCTCTGCAATTGTAATGAGCCTGTTGGGGTACAGATAAATTGAGAACAGGAAACACATTGAATTTCATTCAACCAGTTGCAAAGCTGAAATGAGCCCCAGTGAGGTAGGAAACTGCCCCATTGAACGCTTCCCTCGCTATTGAACTAATTGAACTTGTATAAAACACCAAAACCTGCTCACT

## **FIGURE 142**

MLLLLLEYNFPIENNQHLKTTHTFRVKNLNPKKFSIHQDHKVLVLDGNLIAVPDKNYIRPEI  
FFALASSLSSASAEGSPILLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAQKESARRPFI  
FYRAQVGSWNMLESAAHPGWFICTSCNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD

cAMP- and cGMP-dependent protein kinase phosphorylation site.  
amino acids 33-36

N-myristoylation site.  
amino acids 50-55, 87-92

Interleukin-1  
amino acids 37-182

## **FIGURE 143**

CTAGAGAGTATAGGGCAGAAGGATGGCAGATGAGTGACTCCACATCCAGAGCTGCCTCCCTTAA  
TCCAGGATCCTGTCCTCCTGTCCTGTAGGAGTGCCTGTTGCCAGTGTGGGTGAGACAAGTTG  
TCCCACAGGGCTGTCAGCAGATAAGATTAAGGGCTGGGTCTGTGCTCAATTAACTCCTGTGG  
CACGGGGCTGGGAAGAGCAAAGTCAGCGGTGCCTACAGTCAGCACCAATGCTGGCCTGCCGTGG  
AAGGGAGGTCTGTCCTGGCGCTGCTGCTCTCTTAGGCTCCAGATCCTGCTGATCTATGC  
CTGGCATTTCACGAGCAAAGGACTGTGATGAACACAATGTCATGGCTCGTTACCTCCCTGCCA  
CAGTGGAGTTGCTGTCACACATTCAACCAACAGAGCAAGGACTACTATGCCTACAGACTGGGG  
CACATCTGAATTCTGGAAGGAGCAGGTGGAGTCCAAGACTGTATTCTCAATGGAGCTACTGCT  
GGGGAGAACTAGGTGTGGAAATTGAAAGACGACATTGACAACACTGCCATTCCAAGAAAGCACAG  
AGCTGAACAATACTTACCTGCTTCTCACCATCAGCACCAAGGCCCTGGATGACTCAGTTCAGC  
CTCCTGAACAAGACCTGCTGGAGGGATTCCACTGAGTGAACCCACTCACAGGCTTGTCATGT  
GCTGCTCCCACATTCCGTGGACATCAGCACTACTCTCCTGAGGACTCTCAGTGGCTGAGCAGCT  
TTGGACTTGTGTTATCCTATTTGCATGTGTTGAGATCTCAGATCAGTGTAGTTAGAAAATCC  
ACACATCTGAGCTAATCATGTAGTGTAGATCATTAAACATCAGCATTAAAGAAAAAAAAAAAA  
AA

## **FIGURE 144**

MLGLPWKGGLSWALLLLLLGSQILLIYAWHFHEQRDCDEHNVMARYLPATVEFAVHTFNQQSKDY  
YAYRLGHILNSWKEQVESKTVFSMELLGRTRCGKFEDDIDNCHFQESTELNNTFTCFFTISTRP  
WMTQFSLLNKTCLEGFH

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 117-121, 139-143

**N-myristylation site.**

amino acids 9-15

## **FIGURE 145**

CTGTGCAGCTCGAGGCTCCAGAGGCACACTCCAGAGAGAGCCAAGGTTCTGACCGGATGAGGAAG  
CACCTGAGCTGGTGGCTGGCACTGTCTGCATGCTGCTCTTCAGCCACCTCTGCGGTCCA  
GACGAGGGGCATCAAGCACAGAATCAAGTGGAACCGGAAGGCCCTGCCAGCACTGCCAGATCA  
CTGAGGCCAGGTGGCTGAGAACCGCCGGAGCCTCATCAAGCAAGGCCAGCTGACATT  
GACTTCGGAGCCGAGGGCAACAGGTACTACGAGGCCAACTACTGGCAGTTCCCCGATGGCATCCA  
CTACAACGGCTGCTTGAGGCTAATGTGACCAAGGAGGCATTGTCACCGGCTGCATCAATGCCA  
CCCAGGCGCGAACCCAGGGGGAGTCCAGAACGCCAGAACACAAGCTCCACCAGCAGGTGCTCTGG  
CGGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTGGTGGAGAGGGCGCAGGACT  
TCGGGTACCATGCACCAGCCAGTGCCTCTGCCTTCTGGCTTGATCTGGCTCATGGTGAAAAT  
AAGCTTGCACGGAGGCTGGCAGTACAGAGCGCAGCGAGCAAATCCTGGCAAGTGACCCAGCT  
CTTCTCCCCAAACCCACGCGTGTCTGAAGGTGCCAGGAGCGCGATGCACACTCGCACTGCAA  
TGCCGCTCCCACGTATGCGCCCTGGTATGTGCCTGCCTGATAGATGGGGACTGTGGCTTCT  
CCGTCACCCATTCTCAGCCCCAGCAGCGTCTGGCACACTAGATTAGTAGTAAATGCTTGAT  
GAGAAGAACACATCAGGCAGTGCAGGCCACCTGCTCACAGTACTTCCAACAACTCTAGAGGTAG  
GTGTATTCCCCTTACAGATAAGGAAACTGAGGCCAGAGAGCTGAAGTACTGCACCCAGCATC  
ACCAGCTAGAAAGTGGCAGAGCCAGGATTCAACCCCTGGCTTGCTAACCCAGGTTCTGCTCT  
GTCCAATTCCAGAGCTGTCTGGTGAATCACTTATGTCTCACAGGGACCCACATCAAACATGTAT  
CTCTAAATGAAATTGTGAAAGCTCCATGTTAGAAATAATGAAAACACCTGA

## **FIGURE 146**

MRKHLSWWLATVCMLLFSHL SAVQTRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQGRK  
LDIDFGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQAANQGEFQKPDNLHQQ  
VLWRLVQELCSLKHC EFWLERGAGL RVTMHQPVLLCLLALIWL MVK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 157-171

**N-glycosylation sites.**

amino acids 98-102, 110-114

**Tyrosine kinase phosphorylation site.**

amino acids 76-83

**N-myristoylation sites.**

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

**Amidation site.**

amino acids 62-66

### **FIGURE 147**

GCCTTGGCCTCCAAAGGGCTGGGATTATAGGCGTGACCACCATGTCGGTCCAGAGTCTCATTT  
CCTGATGATTTATAGACTCAAAGAAAACTCATGTTCAGAAGCTCTCTTCTGGCCTCCTCT  
CTGTCTTCTTCCCTTTCTTCTTATTAAATTAGTAGCATCTACTCAGAGTCATGCAAGCTGG  
AAATCTTCATTTGCTGTCAGGGGTAGGTCACTGAGTCTTAGTTTTATTTTGAAATT  
CAACTTCAGATTCAAGGGGTACATGTGAAGGTTGTTTATGAGTATATTGCATGATGCTGAGG  
TTTGGGGT

## **FIGURE 148**

MFRSSLLFWPPLCLLSLFLLILISSIYSESCKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGTCE  
GLFYEYIA

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-myristoylation site.**

amino acids 62-68

## **FIGURE 149**

GTCTCCGCGTCACAGGAACCTCAGCACCCACAGGGCGGACAGCGCTCCCTCTACCTGGAGACTTGAC  
TCCCAGCGCCCCAACCTGCTTATCCCTGACCGTCGAGTGTAGAGATCCTGCAGCCGCCAGTCC  
CGGCCCCCTCTCCGCCCCAACCCACCCCTCGCTCTTCTGTTTACTCCTCTTCAATTCTATA  
ACAAAAGCTACAGCTCCAGGAGCCAGCGCCGGCTGTGACCCAAGCCAGCGTGGAAAGAATGGGGTT  
CCTCGGGACCGGCACTTGGATTCTGGTGTAGTGTCCCATTCAAGCTTCCCCAACCTGGAGGAA  
GCCAAGACAAATCTACATAATAGAGAATTAAAGTCAGAAAGACCTTGAATGAACAGATTGCTGAA  
GCAGAAGAAGACAAGATTAAAAAACATATCCTCAGAAAACAAGCCAGTCAGAGCAACTATTCTT  
TGTTGATAACTTGAACCTGCTAAAGCAATAACAGAAAAGGAAAAATTGAGAAAGAAAGACAATCTA  
TAAGAAGCTCCCCACTTGATAATAAGTTGAATGTGGAAAGATGTTGATTCAACCAAGAATCGAAAATG  
ATCGATGATTATGACTCTACTAAAGATGGATGGATCATAAATTCAAGATGATCCAGATGGTCTCA  
TCAACTAGACGGGACTCCTTAACCGCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTATGAAG  
AAAATGACAGAGCCGTGTTGACAAGATTGTTCTAAACTACTTAATCTGGCCTTATCACAGAAAGC  
CAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTACAAAATTAACTCAAGGAAGCCAAACAA  
TTATGAGGAGGATCCAATAAGCCCACAAGCTGGACTGAGAATCAGGCTGGAAAAATACCAGAGAAAG  
TGACTCCAATGGCAGCAATTCAAGATGGCTTGCTAAGGGAGAAAAGATGAAACAGTATCTAACACA  
TTAACCTTGACAAATGGCTTGGAAAGGAGAACTAAACCTACAGTGAAGACAACTTGAGGAACCTCA  
ATATTTCCAAATTCTATGCCTACTGAAAGTATTGATTCAAGAAAAGCAAAAGAGAAAGAAA  
CACTGATTACTATCATGAAAACACTGATTGACTTGTGAAGATGATGGTGAATATGGAACAATATCT  
CCAGAAGAAGGTGTTCTACCTTGAAACTTGGATGAAATGATTGCTCTCAGACCAAAACAAGCT  
AGAAAAAAATGCTACTGACAATATAAGCAAGCTTCCAGCACCCTAGAGAAGAGTCATGAAGAAA  
CAGACAGTACCAAGGAAGAAGCAGCTAAGATGGAAAAGGAATATGGAAGCTGAAAGGATTCCACAAAA  
GATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAACAGAACCTATTGGAAGC  
CATCAGAAAAAATATTGAATGGTGAAGAAACATGACAAAAGGAAATAAAGAAGATTATGACCTT  
CAAAGATGAGAGACTTCATCAATAAAACAGCTGATGCTTATGTGGAGAAAGGCATCCTGACAAGGAA  
GAAGCCGAGGCCATCAAGCGCATTATAGCAGCCTGTAAAATGGCAAAAGATCCAGGAGTCTTCAA  
CTGTTTCAAGAAAACATAATATAGCTTAAACACTTCAATTCTGTGATTAAAATTTTGACCCAAGG  
GTTATTAGAAAGTGTGAATTACAGTAGTTAACCTTACAAGTGGTTAAAACATAGCTTCTTCCC  
GTAAAAACTATCTGAAAGTAAAGTTGTATGTAAGCTGAAAAAAAAAAAAAAAAAAA

## **FIGURE 150**

MGFLGTGTWILVLVLPIQAFPKPGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPENKPG  
QSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTKSGLDHK  
FQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFHKIVSKLLNLGLITESQAHTLEDEVAE  
VLQKLISKEANNYEEDPNKPTSWTENQAGKIPKEKVTMMAIQDGLAKGENDETVSNTLTLTNGL  
RRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKMMVKYGTISPEEGV  
SYLENLDEMIALQTKNKNATDNISKLFPAPEKSHEETDSTKEEAAKMEKEYGSLKDSTKDD  
NSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGKEDYDLSKMRDFINKQADAYVEKGILD  
EEAEAIKRIYSSL

**N-glycosylation sites:**

amino acids 68-71, 346-349, 350-353

**Casein kinase II phosphorylation site:**

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-  
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-  
341, 369-372, 382-385, 386-389, 387-390

**N-myristoylation sites:**

amino acids 143-148, 239-244

## **FIGURE 151**

CGGCTCGAGGCTCCGCCAGGAGAAAGGAACATTCTGAGGGGAGTCTACACCCGTGGAGCTCAA  
**GATGGT**CCTGAGTGGGGCCTGTGCTTCCGAATGAAGGACTCGGCATTGAAGGTGCTTATCTGC  
ATAATAACCAGCTCTAGCTGGAGGGCTGCATGCAGGGAAAGTCATTAAGGTGAAGAGATCAGC  
GTGGTCCCCAATCGTGGCTGGATGCCAGCCTGCCCCGTATCCTGGGTGTCAGGGTGGAAAG  
CCAGTGCCTGTCACTGGGGTGGGCAGGAGCCACTCTAACACTAGAGCCAGTGAACATCATGG  
AGCTCTATCTGGTGCAGGAATCCAAGAGCTTCACCTCTACCCGGGGACATGGGGCTCACC  
TCCAGCTCGAGTCGGCTGCCTACCCGGCTGGTCTGTGACGGTGCCTGAAGCCGATCAGCC  
TGTCACTCACCAGCTCCCGAGAATGGTGGCTGGAAATGCCCATCACAGACTTCACTTCC  
AGCAGTGTGACTAGGGCAACGTGCCCCCAGAACTCCCTGGGCAGAGCCAGCTCGGGTGAGGGT  
GAGTGGAGGAGACCATGGCGGACAATCACTCTCTGCTCTCAGGACCCCCACGTCTGACTTAG  
TGGGCACCTGACCACTTGTCTCTGGTCCCAGTTGGATAAATTCTGAGATTGGAGCTCAGT  
CCACGGTCCTCCCCACTGGATGGTGCTACTGCTGTGAACTTGTAAAAACCATGTGGGTAAA  
CTGGGAATAACATGAAAAGATTCTGTGGGGTGGGGAGTGGTGGGAATATTCTGCT  
TAATGGTAACTGACAAGTGTACCTGAGCCCCGCAGGCCAACCATCCCCAGTTGAGCCTATA  
GGGTCACTAGCTCCACATGAAGTCTGTCACTCACCAGTGTGCAAGGAGAGGGAGGTGGTCATA  
GAGTCAGGGATCTATGGCCCTTGGCCAGCCCCCACCCCTTAAATCCTGCCACTGTCTATA  
TGCTACCTTCTATCTTCCCTCATCATCTTGTGTTGGCATGAGGAGGTGGTGTGAGTGT  
GAAATGGCTCGAGCTCAGAAGATAAAAGATAAGTAGGGTATGCTGATCCTTTAAAAACCAA  
GATACAATCAAATCCCAGATGCTGGTCTATTCCATGAAAAAGTGTCTGACATATTGAGA  
AGACCTACTTACAAAGTGGCATATAATTGCAATTATTAAAGATAACCTATTATATT  
TCTTTATAGAAAAAAAGTCTGGAAGAGTTACTTCAATTGTAGCAATGTCAAGGTGGCAGTAT  
AGGTGATTCTTAAATTCTGTTAAATTCTGTTAACTCTGATTCTCTAAATTCTACAATGAAGATGA  
ATTCCCTGTATAAAATAAGAAAAGAAATTATCTGAGGTAAAGCAGAGCAGACATCATCTG  
TTGTCCTCAGCCTCCACTTCCCAGAGTAAATTGAAATCGAGCTGCTGCTCTGGTTGG  
TTGTTAGTAGTGTGATCAGGAAACAGATCTCAGCAAAGCCACTGAGGAGGAGGCTGTGCTGAGTTGT  
GTGGCTGGAATCTCTGGTAAGGAACCTTAAAGAACAAGGAACTTAAAGAAGGCTGCTGTACTGGTTGA  
GATCACAGCCCCCTGGGATTCCAAGGCATTGGATCCAGTCTTAAGAAGGCTGCTGTACTGGTTGA  
ATTGTGCCCCCTCAAATTACATCCTCTTGGAAATCTCAGTCTGTGAGTTATTGGAGATAAG  
GTCTCTGCAAGATGTAGTTAGTTAAGACAAGGTCACTGCTGGATGAAGGTAGACCTAAATTCAATAT  
GACTGGTTCTGTATGAAAAGGAGGGACACAGAGACAGAGGAGACGCGGGGAAGACTATGTA  
AAGATGAAGGAGCAGAGTCGGAGTTTGCAGCCACAAGCTAAGAAACACCAAGGATTGTGGCAACC  
ATCAGAAGCTTGGAAAGAGGCAAAGAAGAATTCTCCCTAGAGGTTAGAGGGATAACGGCTCTG  
CTGAAACCTTAATCTCAGACTTCCAGCCTCTGAACGAAGAAAGAATAATTCCGGCTGTTTAA  
GCCACCAAGGATAATTGGTTACAGCAGCTTAGGAAACTAATACAGCTGCTAAATGATCCTGT  
CTCCTCTGTTACATTCTGTGTGTGCCCCCTCCACATGTACCAAAGTTGTCTTGACCAA  
TAGAATATGGCAGAAGTGTGATGCCACTTCCAAGATTAGGTTATAAAAGACACTGCAGCTTC  
TACTTGAGCCCTCTCTCTGCCACCCACGGCCCCAATCTATCTGGCTCACTCGCTCTGGGG  
AAGCTAGCTGCCATGCTATGAGCAGGCCTATAAGAGACTTACGTGGTAAAAAATGAAGTCTCCT  
GCCACAGCCACATTAGTGAACCTAGAAGCAGAGACTCTGTGAGATAATCGATTTGTTGTTTAA  
AAGTTGCTCAGTTGGTCTAATTGTTATGCAGCAATAGATAAAATATGCAGAGAAAGAG

## **FIGURE 152**

MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEIISVVPNRWLDASLSPVILGVQGGS  
QCLSCGVGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTVPEADQP  
VRLTQLPENGGWNAPITDFYFQQCD

**N-myristoylation sites.**

amino acids 29-34, 30-35, 60-65, 63-68, 73-78, 91-96, 106-111

**Interleukin-1 signature.**

amino acids 111-131

**Interleukin-1 proteins.**

amino acids 8-29, 83-120, 95-134, 64-103

## **FIGURE 153**

CTTCAGAACAGGTTCTCCTCCCCAGTCACCAGTTGCTCGAGTTAGAATTGTCTGCAATGGCCGC  
CCTGCAGAAATCTGTGAGCTTTCTTATGGGACCCGGCCACCAGCTGCCTCCTCTCTGG  
CCCTCTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCACTGCAGGCTTAGCTGGCTGACAAGTCAAAC  
TTCCAGCAGCCCTATATCACCAACCGCACCTCATGCTGGCTAAGGAGGCTAGCTTGGCTGATAA  
CAACACAGACGTTCTCATGGGAGAAACTGTTCCACGGAGTCAGTATGAGTGAGCGCTGCT  
ATCTGATGAAGCAGGTGCTGAACCTCACCCCTGAAGAAGTGCTGTTCCCTCAATCTGATAGGTT  
CAGCCTATATGCAGGGAGGTGGTGCCTCTGGCCAGGCTCAGCAACAGGCTAACGACATGTCA  
TATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAAAAGC  
TTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTGGATTGCTGTTATGTCCTGAGAAAT  
GCCTGCATTTGACCAAGAGCAAAGCTGAAAAATGAATAACTAACCCCTTCCCTGCTAGAAATAA  
CAATTAGATGCCCAAAGCGATTTTTAACAAAAGGAAGATGGAAAGCCAAACTCCATCATG  
ATGGGTGGATTCCAAATGAACCCCTGCGTTAGTTACAAAGGAAACCAATGCCACTTTGTTATA  
AGACCAGAAGGTAGACTTCTAAGCATAGATTTATTGATAACATTGTAACTGGTGTTC  
TATACACAGAAAACAATTATTAAATAATTGTCTTTCCATAAAAAAGATTACTTTCCAT  
TCCTTAGGGAAAAACCCCTAAATAGCTCATGTTCCATAATCAGTACTTATATTATAAA  
TGTATTATTATTATTATAAGACTGCATTTATTATCATTAAATATGGATTATTAT  
AGAAACATCATTGATATTGCTACTTGAGTGTAAAGGCTAATATTGATATTATGACAATAATTAT  
AGAGCTATAACATGTTATTGACCTCAATAAACACTGGATATCCC

## **FIGURE 154**

MAALQKVSSFLMGTLATSCLLLALLVQGGAAAPISSHCRLDKSNFQQPYITNRTFMLAKEASL  
ADNNNTDVRLLIGEKLFHGVSMERCYLMQVLFNFTLEEVLFQSDRFQPYMQUEVVPFLARLSNRLS  
TCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

**Important features of the protein:**

**Signal peptide:**

amino acids 1-33

**N-glycosylation sites.**

amino acids 54-58, 68-72, 97-101

**N-myristoylation sites.**

amino acids 14-20, 82-88

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 10-21

## **FIGURE 155**

GGCTTGCTGAAAATAAAATCAGGACTCCTAACCTGCTCCAGTCAGCCTGCTTCCACGAGGCCTGT  
CAGTCAGTGCCCGACTTGTGACTGAGTGTGAGTCAGTGCAGTGCCTCAGCATGTACCGAGGTCAAGTGCAGAGGGC  
TGCCTGAGGGCTGTGCTGAGAGGGAGAGGAGCAGAGATGCTGCTGAGGGTGGAGGGAGGCCAAGC  
TGCCAGGTTGGGCTGGGGCAAGTGGAGTGAGAAACTGGATCCCAGGGGAGGGTGCAGAT  
GAGGGAGCACCCAGATTAGGTGAGGACAGTTCTCTCATTAGCCTTCTACAGGTGGTTGCAT  
TCTTGGCAATGGTCATGGGAACCCACACCTACAGCCACTGGCCAGCTGCTGCCAGCAAAGGG  
CAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCTGTGCCTCCCTAGAGCCTGCTAG  
GCCCAACCGCCACCCAGAGTCCTGTAGGGCCAGTGAAGATGGACCCCTAACAGCAGGGCCATCT  
CCCCCTGGAGATATGAGTTGGACAGAGACTGAAACCGGCTCCCCAGGACCTGTACCAACGCCCGT  
TGCCTGTGCCCGACTGCGTCAGCCTACAGACAGGCTCCACATGGACCCCGGGCAACTCGGA  
GCTGCTCTACCACAAACCAGACTGTCTTCTACAGGCGGCCATGCCATGGCGAGAAAGGGACCCACA  
AGGGCTACTGCCTGGAGCGCAGGCTGTACCGTGTTCCTAGCTTGTGTGTGCAGGGCCCGT  
GTGATGGGCTAGCCGGACCTGCTGGAGGCTGGTCCCTTTGGAAACCTGGAGCCAGGTGTACA  
ACCACTGCCATGAAGGGCCAGGATGCCAGATGCTGGCCCTGTGAAGTGCTGTGGAGCAG  
CAGGATCCCGGGACAGGATGGGGGCTTGGGAAAACCTGCACTTCTGCACATTGAAAAGAG  
CAGCTGCTGCTAGGGCCGCCAGCTGGTGTCTGTCAATTCTCTCAGGAAAGGTTTCAA  
GTTCTGCCATTCTGGAGGCCACCACTCCTGTCTTCCCTTTCCATCCCTGCTACCTG  
GCCCAGCACAGGCACTTCTAGATATTCCCCCTGCTGGAGAAGAAAAGAGCCCTGGTTTATT  
TGTGTTGTTACTCATCACTCAGTGAGCATCTACTTGGGTGCATTAGTGTAGTTACTAGCTT  
TTGACATGGATGATTCTGAGGAGGAAGCTGTTATTGAATGTATAGAGATTATCCAATAAATAT  
CTTTATTTAAAAATGAAAAA

## **FIGURE 156**

MRERPRLGEDSSLISLFLQVVAFLAMVMGHTHTYSHWPSCCPGQDTSEELLRWSTVPVPPLEPA  
RPNRHPESCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPRGNS  
ELLYHNQTVFYRRPCHGEKGTHKGYCLERRLYRVSLACVCVRPRVMG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-32

**N-glycosylation site.**

amino acids 136-140

**Tyrosine kinase phosphorylation site.**

amino acids 127-135

**N-myristoylation sites.**

amino acids 44-50, 150-156

## **FIGURE 157**

CCGGCG**GATG**TCGCTCGTGCTGCTAACGCTGGCCGCGCTGTGCAGGAGCGCCGTACCCGAGAGCC  
GACCGTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCC  
CCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACTAGTGTGCAACAGGGACTATTCA  
ATTTGATGAATGTAAGCTGGGTACTCCGGCAGATGCCAGCATCCGCTTGTGAAGGCCACCAA  
GATTTGTGTGACGGCAAAGCAACTCCAGTCAGCTGTGAGGTGCAATTACACAGAGG  
CCTTCCAGACTCAGACCAGACCCCTGGTGGTAAATGGACATTTCTACATCGGCTTCCCTGTA  
GAGCTGAACACAGCTATTCATTGGGCCATAATATTCTTAATGCAAATATGAATGAAGATGG  
CCCTTCCATGTCGTGAATTTCACCTCACCAAGGCTGCCTAGACCACATAATGAAATATAAAAAAA  
AGTGTGTCAAGGCCGAAGCCTGTGGATCCGAACATCACTGCTGTGAAAGAAGATGAGGAGACA  
GTAGAAAGTGAACCTCACACCACCTCCCTGGAAACAGATACTGGCTTATCCAACACAGCAC  
TATCATGGGTTTCAGGTGTTGAGCCACACCAGAAAGAAACAAACGCGAGCTTCAGTGGTGA  
TTCCAGTGACTGGGATAGTGAAGGTGCTACGGTCAGCTGACTCCATATTCTACTTGTGGC  
AGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCACAAACAGGCGTCCCTTCCCT  
GGATAACAAACAAAGCAAGCCGGGAGGCTGGCTGCCTCTCCTGCTGCTCTGCTGGTGGCCA  
CATGGGTGCTGGTGGCAGGGATCTATCTAAAGGTTCTGTGGTTACCCATCTGAAATATGTTCCA  
TCTACCACCAACTACTGCCCTCATTAAGGTTCTGTGGTTACCCATCTGAAATATGTTCCA  
TCACACAATTGTTACTTCACTGAATTCTCAAAACCATTGCAGAAGTGAGGTGACTCTGAAA  
AGTGGCAGAAAAGAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTGCCACTCAAAGAAGGCA  
GCAGACAAAGTCGCTTCCTTCCAATGACGTCAACAGTGTGCGATGGTACCTGTGGCAA  
GAGCGAGGGCAGTCCAGTGAGAACTCTCAAGACCTCTCCCCCTGCCTTAACCTTCTGCA  
GTGATCTAAGAAGCCAGATTCTGACAAATACGTGGTGGCTACTTAGAGAGATTGATACA  
AAAGACGATTACAATGCTCTCAGTGTCTGCCCAAGTACCCACCTCATGAAGGATGCCACTGCTT  
CTGTGCAAGAACATTCTCCATGTCAAGCAGCAGGTGTCAGCAGGAAAAGATCACAAGCCTGCCACG  
ATGGCTGCTGCTCCTTGTAG

## **FIGURE 158**

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLIPGDLRDLRVEPVTTSVATGDYSILMNWSV  
LRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGFPVELNTVYFIGAHNIP  
NANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKAGSLWDPNITACKNEETVEVNFTTPIGLNRYMAIQH  
STIIGFSQVFEPHQKKQTRASVVIPTGDSSEGATVQLTPYFPTCGSDCIRHKGTVVLCPQTGVFPFLDNNK  
SKPGGWLPLLLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTLLPPIKVLVVPSEICFHHTICYFTEFL  
QNHCRSEVILEKWQKKIAEMGPVQWLATQKKAADKVVFLSNDVNSVCDGTCGKSEGSPSENSQDLFPLA  
FNLFCSDLRSQIHLHKYVVVYFREIDTKDDYNALSVCPKYHLMKDATAFCAELLHVKKQVSAGKRSQACHD  
GCCSL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-14

**Transmembrane domain:**

amino acids 290-309

**N-glycosylation sites.**

amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201 and 283  
- 287

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 228 - 232 and 319 - 323

**Casein kinase II phosphorylation sites.**

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

**N-myristoylation site.**

amino acids 116-122

**Amidation site.**

amino acids 488-492

## **FIGURE 159**

AGCCACCAGCGAACATGACAGTGAAGACCC~~T~~GCATGGCC~~C~~AGCCATGGTCAAGTACTTGCTGCT  
GTCGATATTGGGGCTTGCCTTCTGAGTGAGGCGGCAGCTCGGAAAATCCCCAAAGTAGGACATA  
CTTTTTCCAAAAGCCTGAGAGTTGCCGCCGTGCCAGGAGGTAGTATGAAGCTTGACATTGGC  
ATCATCAATGAAAACCAGCGCGTTCCATGTCACGTAACATCGAGAGCCGCTCACCTCCCCCTG  
GAATTACACTGTCACTGGGACCCCAACC~~G~~GTACCCCTCGGAAGTTGTACAGGCCAGTGTAGGA  
ACTTGGGCTGCATCAATGCTCAAGGAAAGAACATCTCCATGAATTCCGTTCCATCCAGCAA  
GAGACCTGGTCGTCGGAGGAAGCACCAAGGCTGCTCTGTTCTTCCAGTTGGAGAAGGTGCT  
GGTGACTGTTGGCTGCACCTGCGTCACCCCTGT~~C~~ATCCACCATGTGCAGTAAGAGGTGCATATCC  
ACTCAGCTGAAGAAG

## **FIGURE 160**

MTVKTLHGPAMVKYLLSILGLAFLSEAAARKIPKVGHFFQKPESC PPPVPGGSMKLDIGIINEN  
QRVSMSRNIESRSTSPWNYTVTWDPNRYPSEVVQAQCRLGCINAQGKEDISMNSVPIQQETLVV  
RRKHQGCSVSFQLEKVLVTVGCTCVTPVIHHVQ

**Signal sequence:**

amino acids 1-30

**N-glycosylation site.**

amino acids 83-87

**N-myristoylation sites.**

amino acids 106-111, 136-141

### **FIGURE 161**

ACACTGGCCAAACAAAAACGAAAGCACTCCGTGCTGGAAGTAGGAGGAGAGTCAGGACTCCCAAG  
ACAGAGAGTGACAAACTACCCAGCACAGCCCCCTCCGCCCCCTCTGGAGGCTGAAGAGGGATT  
CAGCCCCCTGCCACCCACAGACACGGGCTACTGGGTGCTGCCCTCTGGGGGGGGCAGCAC  
AGGGCCTAGGCTGGGTGCCACCTGGCACCTAGAAGATGCTGTGCCCTGGTTCTGCTGTCT  
TGGCACTGGGCCGAAGCCAGTGGCTTTCTGGAGGAGGCTTGTGGGGCTCAGGACGCTACC  
CACTGCTCTCGGGCTCTCTGGCCTCTGGACAGTGACATACTCTGCCCTGGGACAT  
CGTGCCTGCTCCGGGCGTGTGGCGCTACGCACCTGCAGACAGAGCTGGTGTGAGGTGCC  
AGAAGGAGACCGACTGTGACCTCTGCTCGGTGTGGCTGTCCACTTGGCGTGCATGGCACTGG  
GAAGAGCCTGAAGATGAGGAAAAGTTGGAGGAGCAGCTGACTCAGGGTGGAGGAGCCTAGGAA  
TGCCTCTCCAGGCCAAGTCGTCTCTCCAGGCCAACCTACTGCCGCTGCGTCTGC  
TGGAGGTGCAAGTGCCTGCTGCCCTGTGCAGTTGGTCACTGTGTGGCTCTGTTGATATGAC  
TGCTTCGAGGCTGCCCTAGGGAGTGAACATCTGGTCTATACTCAGGCCAGGTACGAGAA  
GGAACCTAACCAACACAGCAGCTGCCCTGCCCTGGCTAACGTGTCAGCAGATGGTACA  
ACGTGCATCTGGTTCTGAATGTCCTGAGGAGCAGCACTTCGGCCTCTCCCTGACTGGAACTCAG  
GTCCAGGGCCCCCCTAACACCCGGTGGCACAAAACCTGACTGGACCGCAGATCATTACCTTGA  
CCACACAGACCTGGTTCCTGCCCTGTATTCAAGGTGTGGCCTCTGAAACCTGACTCCGTTAGGA  
CGAACATCTGCCCTTCAGGGAGGACCCCCCGCAGCACACCAGAACCTCTGGCAAGCCGCCGACTG  
CGACTGCTGACCCCTGAGAGCTGGCTGCTGGACGCACCGTGTGCTGCCGAGAACGGGCACT  
GTGCTGGGGGCTCCGGTGGGACCCCTGCCAGCAACTGGTCCCACCGCTTCTGGAGAACG  
TCACTGTGGACAAGGTCTCGAGTTCCCATGTGAAAGGGCACCCCTAACCTCTGTGTTCAGGTG  
AACAGCTGGAGAAGCTGAGCTGAGGACTGGCTGTGGCTGACTCCCTGGGGCTCTCAAAGA  
CGATGTGCTACTGTGGAGACAGCAGGCCCCCAGGACACAGATCCCTGTGCTTGGAAACCCA  
GTGGCTGACTTCACTACCCAGAACGCTTCAAGGGCAGCTGCCCTGGAGAGTACTTACTA  
CAAGACCTGCACTGAGGCAAGTGTCTGCAGCTATGGGACGATGACTGGGAGCCTATGGGCTG  
CCCCATGGACAAATACATCCACAAAGCGCTGGGCCCTCGTGTGGCTGCCCTACTCTTGGG  
CTGCGCTTCCCTCATCCTCTCAAAAAGGATCACCGAAAGGGTGGCTGAGGCTTGGTAA  
CAGGACGCTCGCTGGGGGCCAGGGCCGCGCCCTGTGCTGCCCTACTCAGCCGATG  
CTCGGGTTTCAGGCCCTGGTGGCGCCCTGGCTGCCAGCTGCCCTGTGCGCTGGCTGG  
CCGTAGACCTGTGGAGCCGTGAACTGAGCGCGCAGGGGCCCTGGCTTGGTTTACGCCAG  
CGGCGCCAGACCCCTGCAAGGAGGGCGCGTGGTGTGCTTCTCTCCGGTGCCTGGCGCT  
GTGCAAGGAGTGGCTACAGGATGGGTGCTGGGCCGGGCGCACGGCCCGCACGACGCCCTCC  
GCGCCTGCTCAGCTGCGTGCCTGCCGACTTCTGCAAGGGCCGGCGCCGGCAGCTACGTTGGG  
GCCCTGCTTCAGCAGGGCTGCTCACCCGAGCCGTACCCGCCCTTCCGCACCGTGCCCT  
CACACTGCCCTCCCAACTGCCAGACTTCTGGGGCCCTGCAGCAGCCTCGCGCCCCCGCTTCC  
GGCGGCTCCAAGAGAGAGCGGAGCAAGTGTCCCGGGCCCTCAGCCAGCCCTGGATAGCTACTTC  
CATCCCCGGGACTCCCGCAGGGAGCAGGGGGTGGGACCGGGGGGGGACCTGGGGCGGGGG  
CGGGACTAAAGGAGCAGCGTGTGTTTCTAAAAAAA

## **FIGURE 162**

MPVPWFILLSALGRSPVVLSLERLVPQDATHCSPGLSCRILWDSDILCLPGDIVPAPGPVLAPTHLQTELVLRCQKETDCDLCLRVAHVHLAVGHWEPEDEEKFGGAADSGVVEPRNASLQAQVVLFSFOAYPTARCVILLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPRYEKELNHTQQLPALPWLNVSADGDNVHLVLNVEEQHFGLSLYWNQVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQARLRLLTLQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKLEFPLLKGHPNLCVQVNSSEKILQLQECIWLADSLGPLKDDVLLTRGPQDNRSILCALEPSGCTSLPSKASTRAARLGEYLLQDIQSGQCLQLWDDDLGALWACPMKYIHKRWALVWLACLLFAAALSLLLLKKDHAKGWLRLLKQDVRSGAAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAFHQAQRRQTLQEGGVVVLLFSPGAVALCSEWLQDGVSQPGGAHGPDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTPVVFPLPSQLPDFL GALQQPRAPRSGRLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPAGPGAGDGT

**Signal sequence:**

amino acids 1-20

**Transmembrane domain.**

amino acids 453-475

**N-glycosylation sites.**

amino acids 118-121, 186-189, 198-201, 211-214, 238-241, 248-251, 334-337, 357-360, 391-394

**Glycosaminoglycan attachment site.**

amino acids 583-586

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 552-555

**N-myristoylation sites.**

amino acids 107-112, 152-157, 319-324, 438-443, 516-521, 612-617, 692-697, 696-701, 700-705

## **FIGURE 163**

GGGAGGGCTCTGTGCCAGCCCCGATGAGGACGCTGTGACCATTTGACTGTGGGATCCCTGGCT  
GCTCACGCCCTGAGGACCCCTCGGATCTGCTCCAGCACGTGAATTCAGTCCAGCAACTTGA  
AAACATCCTGACGTGGGACAGGGGGCAGAGGGCACCCAGACACGGTCTACAGCATCGAGTATA  
AGACGTACGGAGAGAGGGACTGGGTGGCAAAGAAGGGCTGTCAGGGATCACCCGGAAAGTCCCTGC  
AACCTGACGGTGGAGACGGGCAACCTCACGGAGCTCTACTATGCCAGGGTACCGCT  
GTCAGTGCAGGGGGGGTCAGCCACCAAGATGACTGACAGGTTAGCTCTGCAGCACACTAC  
CCTCAAGCCACCTGATGTGACCTGTATCTCAAAGTGGAGATCGATTCAAGATGATTGTCATCCTA  
CCCCCACGCCAACCGTGCAGGGCATGGCACCCGGCTAACCTGGAAAGACATCTTCATGACCTG  
TTCTACCACTTAGAGCTCCAGGTCAACCGCACCTACCAAATGCACCTTGGAGGGAAAGCAGAGA  
ATATGAGTTCTCGGCCTGACCCCTGACACAGAGTCCCTGGCACCATCATGATTGCGTTCCA  
CCTGGGCAAGGAGAGTGGCCCTACATGTGCCAGTGAGAACACTGCCAGCCGGACATGGACC  
TACTCCTCTCCGGAGCCTCCCTGTTCTCCATGGGCTCTCGTCAGTACTCTGCTACCTGAG  
CTACAGATATGTACCAAGCCGCTGCACCTCCAACTCCCTGAACGTCAGCGAGTCTGACTT  
TCCAGCCGCTGCGCTTCATCCAGGAGCACGTCTGATCCCTGTTGACCTCAGCGGGCCCCAGC  
AGTCTGGCCAGCCTGTCAGTACTCCCAGATCAGGGTCTGGACCCAGGGAGCCCGCAGGAGC  
TCCACAGCGGATAGCCTGTCAGGAGATCACCTACTTAGGGCAGCCAGACATCTCATCCTCCAGC  
CCTCCAACGTGCCACCTCCCCAGATCCTCTCCCACTGTCCTATGCCCAAACGCTGCCCTGAG  
GTCGGGGCCCCATCCTATGCACCTCAGGTGACCCCCGAAGCTCAATTCCATTCTACGCCAAC  
GGCCATCTAAGGTCCAGCCTCCCTATGCCCTCAAGCACTCCGGACAGCTGGCCTCCCT  
CCTATGGGTATGCATGGAAAGGTTCTGGCAAAGAGACTCCCCACTGGGACACTTTCTAGTCTAA  
CACCTTAAGGCTAAAGGTAGCTTCAGAAAGAGCCACAGCTGGAGCTGATTTGAGGTGCCCT  
TTCTCTGCAAGGAGGTGACCTCTGGCTATGGAGGAATCCAAGAAGCAGAAATCATTGCAACCAGC  
CCCTGGGATTGCAACAGAACATCTCACCCAAATGTGTCACACAGTGGGAGGAAGGGACA  
CCACAGTACCTAAAGGGCCAGCTCCCCCTCCCTCAGTCAGATCGAGGGCCACCCCATGTC  
CCTCCCTTGCAACCTCCTCCGGTCCATGTTCCCTCGGCAAGGTCCAAGTCCCTGGGCC  
TGCTGGAGCTCTGTGTGTCAGGAGATGAAGCCAAGGCCAGGGCTGAGACCTCAGACCTG  
GAGCAGCCCACAGAACACTGGATTCTCTGGCTAGGGCTGGCCCTGACTGTGCAAGGGAGTCTG  
AGGGGAATGGGAAAGGCTGGTCTCTCCCTGTCCTACCCAGTGTCACTCCTGGCTGTCA  
ATCCCATGCCCTGCCATGCCACACACTCTGCGATCTGGCCTCAGACGGGTGCCCTGAGAGAAGC  
AGAGGGAGTGGCATGCAGGGCCCTGCCATGGGTGCGCTCCTCACCGAACAAAGCAGCATGATA  
AGGACTGCAAGGGGGAGCTCTGGGAGCAGCTGTGTAGACAAGCGCTGCTCGCTGAGCCCTG  
CAAGGCAGAAATGACAGTGCAGGAGGAATGCAGGGAAACTCCGAGGTCCAAGGCCACCTC  
CTAACACCATGGATTCAAAGTGCAGGGAAATTGCTCTGCCCTGCTCTGTCAATTGTTCAAAGGTGGGAAGAGA  
GCCAGGGAAAGAACCCAGGCCAGGGAAAGAACAGAAGGAGGCTGGCAGAACCCAGAACACCTG  
ACTTCTGCCAAGGCCAGGGCCAGCAGGACGGACTCTAGGGAGGGGTGTGCCCTGCAGCTCA  
TTCCCAAGGCCAGGGCAACTGCCCTGACGTTGACGTTCAGCTTCATTCTCTGATAGAACAAAGC  
GAAATGCAGGTCCACCAAGGGAGGGAGACACACAAGCCTTTCTGCAGGCAGGAGTTGAGACCCCT  
ATCCTGAGAATGGGGTTGAAAGGAAGGTGAGGGCTGTGGCCCTGGACGGTACAATAACACAC  
TGTACTGATGTACAACATTGCAAGCTCTGCTGGGTTCAGCCCATCTGGCTCAAATTCCAGC  
CTCACCACTCACAAGCTGTGTGACTTCAAACAAATGAAATCAGTGCCAGAACCTCGGTTCCCTC  
ATCTGTAATGTGGGGATCATAACACCTACCTCATGGAGTTGTGGTAAGATGAAATGAAGTCATG  
TCTTAAAGTCTTAATAGTGCCTGGTACATGGCAGTGCCTAAACGGTAGCTATTAAAAA  
AAAAAAA

## **FIGURE 164**

MRTLLTILTVGSLAAHAPEDPSDLLQHVKFQSSNFENILTWDSGPEGTPDTVYSIEYKTYGERDW  
VAKKGCQRITRKSCNLTVEGNLTLYYARVTAVSAGGRSATKMTDRFSSLQHTTLKPPDVT CIS  
KVRSIQMIVHPTPTPIRAGDGHRLTLEDIFHDLFYHLELQVNRTYQMHLGGKQREYEFFGLTPDT  
EFLGTIMICVPTWAKESAPYMCRVKTLPDRTWTYSFGAFLFSMGFLVAVLCYLSYRYVTKPPAP  
PNSLNQVRVLTQPLRFIQEHVLIPVFDLSGPSSLAQPVQYSQIRVSGPREPAGAPQRHSLSEIT  
YLGQPDISILQPSNVPPPQILSPLSYAPNAAPEVGPPSYAPQVTPEAQFPFYAPQAISKVQPSY  
APQATPDSWPPSYGVCMEGSGKDSPTGTLSSPKHLRPKGQLQKEPPAGSCMLGGSLQEVTLAM  
EESQEAKSLHQPLGICTDRTSDPNVLHSGEEGTPQYLGQLPLLSSVQIEGHPMSLPLQPPSGPC  
SPSDQGPSPWGLLESLVCPKDEAKSPAPETSDLEQPTELDSLFRGLALTQWES

**Signal sequence.**

amino acids 1-17

**Transmembrane domain.**

amino acids 233-250

**N-glycosylation sites.**

amino acids 80-83, 87-90, 172-175

**N-myristoylation sites.**

amino acids 11-16, 47-52, 102-107, 531-536, 565-570

## **FIGURE 165**

TGGCCTACTGGAAAAAAAAAAAAAGTCACCCGGGCCCGCGTGGCCACAACATGG  
CTGCGGCGCCGGGGCTGCTCTTCTGGCTGTTCGTGTGGGGCGCTCTGGTGGGTCCCAG  
TCGGATCTCAGCCACGGACGGCGTTCTGGACCTCAAAGTGTGCAGGGACGAAGAGTCAGCAT  
GTTAATGTACCGTGGGAAAGCTTGAAGACTTCACGGCCCTGATTGTCGTTGTGAATT  
AAAAAGGTGACGATGTATATGTTACTACAAACTGGCAGGGGATCCCTGAACCTGGCTGGA  
AGTGTGAACACAGTTGGATATTTCCAAAAGATTGATCAAGGTACTTCATAAATACACGGA  
AGAAGAGCTACATATTCCAGCAGATGAGACAGACTTTGTCGCTTGAGGAGGAAGAGATGATT  
TTAATAGTTATAATGAGAGCTTTAGGATCTTGGAACTGGAGGACTCTGTACCTGAAGAG  
TCGAAGAAAGCTGAAGAAGTTCTCAGCACAGAGAGAAATCTCTGAGGAGTCTCGGGCGTGA  
ACTTGACCCCTGTGCCTGAGCCCGAGGCATTAGCTGAGGACTGATTAGGAGATGGAGAAGGTGCTTCT  
CAGAGAGCACCGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGAGAGCCACCCACACCAGCGGT  
CCTGCCTAAGCTCAGGGAGTGCAGTCTCGTGGACACTTTGAAGAAATTCTGCACGATAA  
ATTGAAAGTGCCGGAAAGCGAAAGCAGAACCTGGCAATAGTTCTCCTGCCTGGAGCAGTGCCTATT  
AGACAGATGCTTACAAAGTCCTGAAAACAGAAATGAGTCAGAGAGGAAGTGGACAGTGCCTATT  
CATTACAGCAAAGGATTCGTTGCATCAAATCTAAGTTGTTACAAAGATTGTTTAGTA  
CTAAGCTGCCTGGCAGTTGCATTTGAGCAAACAAAAATATTATTATTTCCCTCTAAGTA  
AAAAAAAAAAAAAA

## **FIGURE 166**

MAAAPGLLFWLFWLGALWWVPGQSDLSHGRRFSDLKVCGLDEECMILMYRGKALEDFTPDCRFVN  
FKKGDDVYVYYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKYTEELHIPADEDFVCFEGGRD  
DFNSYNVEELLGSLEEDSVPEESKKAAEVSQHREKSPPEESRGRELDPVPEPEAFRADSEDEGA  
FSESTEGLQGQPSAQESHPTSGPAANAQGVQSSLDTFEEILHDKLKVPGSESRTGNSSPASVER  
EKTDAYKVLKTEMSQRGSGQCVIHYSKGFRWHQNLSLFYKDCF

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 294-298

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-34

**Tyrosine kinase phosphorylation site.**

amino acids 67-76

**N-myristoylation sites.**

amino acids 205-211, 225-231, 277-283

**Amidation site.**

amino acids 28-32

## **FIGURE 167**

CCAGGACCAGGGCGCACCGGCTCAGCCTCTACTGTCAGAGGCCGGGAAGAGAACGAAAGCGC  
AACGGTGTGGTCCAAGCCGGGCTCTGCTCGCCTCTAGGACATACACGGGACCCCTAACCTTC  
AGTCCCCAAACGCGCACCTCGAAGTCTTGAACCTCCAGGGCAGACATCCACGCGGGCACAGG  
CGCGCAGGCAGGTCCCAGGCGAAGGCATGCGCGAGGGGGTCGGGCAGCTGGCTCGGGC  
GGCAGGGAGTAGGGCCGGCAGGGAGGCGAGGGAGGCTGCATATTCAAGAGTCGGGCTCGCCCTG  
GGCAGAGGCCGCCCTCGCTCCACGCAACACTGCTGCTGCCACCGCGCCCGATAGCCCGTGG  
TCTCGCTGCTGCTGGCGCCGCGCTGCTCGGCCACGGAGGCTCTGCCGCCGTGGTCAGC  
GCCAAAAGGTGTGTTGCTGACTTCAAGCATCCCTGCTACAAAATGGCTACTTCCATGAAC  
GTCCAGCCGAGTGAAGCTTCAAGGACACGCTGGCTTGAGAGTGAAGGGAGGAGTCCTCA  
GCCTTGAGAATGAAGCAGAACAGAAGTTAATAGAGAGCATGTTGCAAAACCTGACAAAACCCGGG  
ACAGGGATTCTGTGGTATTCTGGATAGGGCTTGGAGGAATGGAGATGGGAAACATCTGG  
TGCCTGCCAGATCTTACCACTGGTCTGTGGAAAGCAATTCCAGTACCGAAACTGGTACACAG  
ATGAACCTCCCTCGGAAAGTGAAGGAAAGTGTGTTGTATGACCAACCAACTGCCAACCTGGC  
CTTGGGGTCCCTACCTTACCACTGGAAATGATGACAGGTGAACATGAAGCACAATTATTTG  
CAAGTATGAAACAGAGATAATCCAACAGCCCTGAGAAAAGCCTATCTTACAATCAACAG  
GAGACACCATGAAATGTGGTGTACTGAAGCAGGTATAATTCCAATCTAATTATGTTGTT  
ATACCAACATACCCCTGCTTACTGATACTGGTTGCTTTGGAAACTGTTGTTCCAGATGCT  
GCATAAAAGTAAGGAAGAACAAAAGTAGTCCAAACCAACTGCTACACTGTGGATTCAAGAGTA  
CCAGAAAAGAAAGTGGCATGGAAGTATAAAACTCATGGACTTGGTCCAGAATTTGTAATTCT  
GGATCTGTATAAGGAATGGCATCAGAACATAGCTGGATGGCTGAAATCAAAGGATCTGC  
AAGATGAACGTAAAGCTCCCCCTGAGGCAAAATTAAAGTAATTATATGCTATTATTTCA  
TTTAAAGAATATGCTGTGCTAAATGGAGTGAGACATGCTTATTTGCTAAAGGATGCCAA  
ACTTCAAACCTCAAGCAAATGAAATGGACATGCAGATAAAAGTTGTTATCAACACGTCGGGAGTA  
TGTGTGTTAGAAGCAATTCTTTATTCTTACCTTCATAAGTTGTTATCTAGTCAATGTA  
TGTATATTGTTAGAATTTACAGTGTGCAAAAGTATTTCACCTTGCTCATAAGTGTGTTGATAAAA  
ATGAACCTGTTCAATATTATTATTGATGGCATCTCATTTCAATACATGCTTTGATTAAAG  
AAACTTATTACTGTTGTCAACTGAATTCACACACACACAAATATACTACCATAGAAAAGTTG  
TTTCTCGAAATAATTCACTTTTACAGTGTGATATAACCTCCCAAACATTACTTAGCTTCA  
AATAAGAAGCTATTCAATTAAAGTGTGATATAACCTCCCAAACATTACTTAGCTTCA  
TGTCTAATTCAATTGTGCAAGACATGTGCTTATAATTATTATTAGCTTAAACAGATT  
TTGTAATTCAATTGTTAATAGGTGCTAAACACTAATGCAATTGCAACAAAAGAAG  
TGACATACACAAATAAAATCATATGTTACACAGTTGCTTATAATGAGAAGCAGCTCTGA  
GGGTTCTGAAATCAATGTGGTCCCTCTTGCCCACTAAACAAAGATGGTTGTTGGGGTTGG  
ATTGACACTGGAGGCAGATAGTGCAGAAAGTTAGCTAAAGGTTCCCTAGCTGTTAGCT  
ACTATATTAGTATACAAAGAGGTCAATGTGGTTGAGACCAAGGTGAATAGTC  
ACAAGCACAGCACACAGACATTAGGAAGGAACACTACGAAATCGTGTGAAAATGGGTTGG  
AACCCATCAGTGATCGCATATTCAATTGATGAGGGTTGCTGAGATAGAAAATGGTGGCTCTT  
CTGTTCTATCTCTAGTTCTCAATGCTTACGCCCTGCTCTCAAGAGAAAGTTGTAAC  
CTGGTCTTCATATGTCCTGCTCCCTTAAACAAATAAAAGAGTTCTGTTCTGGGGAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 168**

MSRVVSLLLGAALLCGHGAFCRVVSGQKVCADFKHPCYK MAY FHELSSRVS FQE ARLACESE  
GGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDFWIGLWRNGDGQTSGACPDLYQWSDGSNSQ  
YRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEINPTAPVEK  
PYLTNQPGDTHQNVVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSKGRTKTSPNQ  
STLWISKSTRKESGMEV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 214-235

**N-glycosylation sites.**

amino acids 86-89, 255-258

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 266-269

**N-myristoylation sites.**

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145, 212-217